

Query Match 100.0%; Score 20; DB 10; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1569 AGGACTCTGAGGCTCTTTCT 1588

RESULT 2

US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,862
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-09-800-909-1

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
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Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 3

US-09-800-908-2
; Sequence 2, Application US/09800908
; Patent No. US20020111462A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,908
; FILING DATE: 08-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,347
; FILING DATE: <Unknown>
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248635
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-800-908-2

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 4

US-09-954-456-1187
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul

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? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
? SEQ ID NO 423
? LENGTH: 480
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AP000046.1
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.4
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
? OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.5
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
US-09-864-761-423

Query Match      84.0%;   Score 16.8;   DB 10;   Length 480;
Best Local Similarity 90.0%;   Pred. No. 21;
Matches 18;   Conservative 0;   Mismatches 2;   Indels 0

Qy      1 AGGACTGTGAGGCTCTTCT 20
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Db      46 AAGACTCTGAAGCTCTTCT 27

RESULT 6
US-09-867-701-6135
? Sequence 6135, Application US/09867701
? Patent No. US20020132237A1
? GENERAL INFORMATION:
? APPLICANT: Aglate, Paul A.
? APPLICANT: Jones, Robert
? APPLICANT: Harlocker, Susan L.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
? FILE REFERENCE: 210121.497
? CURRENT APPLICATION NUMBER: US/09/867,701
? CURRENT FILING DATE: 2001-05-29
? NUMBER OF SEQ ID NOS: 10912
? SOFTWARE: FastSeq for Windows version 4.0
? SEQ ID NO 6135
? LENGTH: 580
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-867-701-6135

Query Match      84.0%;   Score 16.8;   DB 10;   Length 580;
Best Local Similarity 90.0%;   Pred. No. 21;
Matches 18;   Conservative 0;   Mismatches 2;   Indels 0

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; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.1
; OTHER INFORMATION: NT HIT: g111526208, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1801337.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P18583, EVALUE 1.00e-42
US-09-864-761-17120
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Query Match      84.0%; Score 16.8; DB 10; Length 1086;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 AGGACTCTGAGGCTCTTTCT 20
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Db     273 AAGACTCTGAAGCTCTTTCT 254
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RESULT 9

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US-09-864-761-17617/c
; Sequence 17617, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17617
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000114.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.4
; OTHER INFORMATION: EST_HUMAN HIT: A1801337.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: g111526208, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P18583, EVALUE 1.00e-42
US-09-864-761-17617
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Query Match      94.0%; Score 16.8; DB 10; Length 1086;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 AGGACTCTGAGGCTCTTTCT 20
      | | | | | | | | | | | | | | | |
Db     273 AAGACTCTGAAGCTCTTTCT 254
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RESULT 10

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US-09-864-761-12705/c
; Sequence 12705, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12705
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC026236.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.47
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.44
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.47
US-09-864-761-12705

Query Match 80.0%; Score 16; DB 10; Length 526;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCT 16
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DB 434 AGGACTCTGAGGCTCT 419

RESULT 11

US-09-729-835-13/c
; Sequence 13, Application US/09729835
; Patent No. US20010016647A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: P2015P1
; CURRENT APPLICATION NUMBER: US/09/729,835
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/257,179
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/056,270
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,271
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,247
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,073
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: (766)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-729-835-13

Query Match 80.0%; Score 16; DB 10; Length 1336;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTCT 20
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DB 232 AGGAYTTCAGGCTGTCTCT 213

RESULT 12
US-10-002-344A-72
; Sequence 72, Application US/10002344A
; Patent No. US20020172959A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
; FILE REFERENCE: DEX-0241
; CURRENT APPLICATION NUMBER: US/10/002,344A
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/242,998
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-002-344A-72

Query Match 79.0%; Score 15.8; DB 9; Length 239;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTC 19
|||||
DB 219 AGGACTCTGAGGACTTTC 237

RESULT 13

US-10-002-344A-73
; Sequence 73, Application US/10002344A
; Patent No. US20020172959A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
; FILE REFERENCE: DEX-0241
; CURRENT APPLICATION NUMBER: US/10/002,344A
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/242,998
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-002-344A-73

Query Match 79.0%; Score 15.8; DB 9; Length 333;
Best Local Similarity 89.5%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTC 19
|||||
DB 220 AGGACTCTGAGGACTTTC 238

RESULT 14

US-09-867-550-1063
; Sequence 1063, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.

APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby

FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1063
LENGTH: 527
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)..(45)
OTHER INFORMATION: Wherein any n is one of a or t or c or g
US-09-867-550-1063

Query Match 79.0%; Score 15.8; DB 10; Length 527;
Best Local Similarity 89.5%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTC 19
Db 459 AGGTCCTCTGAGGCTCTTGC 477

RESULT 15
US-09-867-550-2118/c
Sequence 2118, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2118
LENGTH: 527
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: reverse complement of SEQ ID NO:1063
NAME/KEY: misc_feature
LOCATION: (484)..(491)
OTHER INFORMATION: Wherein any n may be a or t or g or c
US-09-867-550-2118

Query Match 79.0%; Score 15.8; DB 10; Length 527;
Best Local Similarity 89.5%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTC 19
Db 69 AGGTCCTCTGAGGCTCTTGC 51

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:30:25 : Search time 41.4471 Seconds
(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937A-5
Perfect score: 20
Sequence: 1 tcacagagagtcaggactt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
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- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
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- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
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- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
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- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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C 2	20	100.0	2224	6	ARI52033	ARI52033 Sequence
C 3	20	100.0	2253	6	A78517	A78517 Sequence 1
C 4	20	100.0	2394	9	HUMTNFR11	M55994 Human tumor
C 5	20	100.0	2613	9	HSTNFR2S10	U52165 Human tumor
C 6	20	100.0	3380	11	G26865	G26865 human STS S
C 7	20	100.0	3452	9	S63368	S63368 Homo sapien
C 8	20	100.0	3633	6	AX333705	AX333705 Sequence
C 9	20	100.0	3683	6	AX348016	AX348016 Sequence
C 10	20	100.0	3683	6	AX348018	AX348018 Sequence
C 11	20	100.0	3683	6	AX348020	AX348020 Sequence
C 12	20	100.0	3683	9	HUMNFR	M32315 Human tumor
C 13	20	100.0	115602	9	HS1118D24	AL031276 Human DNA
C 14	20	100.0	122105	2	AL355998	AL355998 Homo sapi
C 15	20	100.0	187877	2	AC023251	AC023251 Homo sapi
C 16	19	95.0	21	12	AB068557	AB068557 Synthetic
C 17	19	95.0	212467	2	AL691472	AL691472 Mus muscu
C 18	19	95.0	213281	2	AL683882	AL683882 Mus muscu
C 19	18.4	92.0	2339	6	A26415	A26415 cDNA fragme
C 20	18.4	92.0	136652	2	AC125086	AC125086 Mus muscu
C 21	18.4	92.0	209877	9	AC012509	AC012509 Homo sapi
C 22	18.4	92.0	333300	2	AC125091	AC125091 Mus muscu
C 23	18	90.0	1124	9	HSCOA8	AJ001544 Homo sapi
C 24	17.4	87.0	92558	9	HS341E18	AL031178 Human DNA
C 25	17.4	87.0	110000	2	LMFLCHR31_01	Continuation (2 of
C 26	17.4	87.0	130338	2	AC104844	AC104844 Oryza sat
C 27	17.4	87.0	139594	2	AC025085	AC025085 Homo sapi
C 28	17.4	87.0	151040	2	AC020827	AC020827 Mus muscu
C 29	17.4	87.0	153926	9	AL160059	AL160059 Human DNA
C 30	17.4	87.0	154109	2	AL108965	AL108965 Rattus no
C 31	17.4	87.0	159384	2	AL356110	AL356110 Homo sapi
C 32	17.4	87.0	160359	2	AC119584	AC119584 Rattus no
C 33	17.4	87.0	166801	2	AC103240	AC103240 Rattus no
C 34	17.4	87.0	169668	2	AL845322	AL845322 Danio rer
C 35	17.4	87.0	172042	2	AC108305	AC108305 Rattus no
C 36	17.4	87.0	185896	2	AC069564	AC069564 Mus muscu
C 37	17.4	87.0	188867	2	AC129341	AC129341 Rattus no
C 38	17.4	87.0	201188	10	AC124169	AC124169 Mus muscu
C 39	17.4	87.0	205883	2	AC102603	AC102603 Mus muscu
C 40	17.4	87.0	221975	2	AC124710	AC124710 Mus muscu
C 41	17.4	87.0	267278	2	AC122252	AC122252 Mus muscu
C 42	17	85.0	20	12	AB068555	AB068555 Synthetic
C 43	17	85.0	2365	9	AK092743	AK092743 Homo sapi
C 44	17	85.0	69631	2	AC126386	AC126386 Homo sapi
C 45	17	85.0	93821	2	AC021596	AC021596 Homo sapi

ALIGNMENTS

RESULT 1
G15915/c

LOCUS human STS CHLC UTR_02819_M32315.870 bp DNA linear STS 19-JAN-1996
DEFINITION sequence tagged site.

ACCESSION G15915.1

VERSION G15915.1

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens vector=pjCpI host=E.coli dut+ung+ (DH10B) Marker

Selected genomic DNA prepared from XY individual of French

nationality.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 870)

AUTHORS Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: UTR_02819_M32315, CHLC_UTR_02819_M32315.T36190
Contact: Dr. Jeffrey C. Murray

UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@iowa.edu

Primer A: CCTGTACCTCTCTGTGACCTG
Primer B: GTCTTCATGGTGACTCAGG
STS size: 206
PCR Profile:

denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C

Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Tag Polymerase: 0.3 units
Total Vol: 10 ul

Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3

Prepared with primer pairs derived from M32315.

Location/Qualifiers

1..870
/organism="Homo sapiens"
/db_xref="taxon:9606"
272..477
272..291
primer_bind complement(458..477)
primer_bind 157 a 246 c 279 g 188 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGGACTT 20
|||||
DB 287 TCACAGAGTCAGGGACTT 268

RESULT 2
AR152033/c AR152033 2224 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 2 from patent US 6232446.
DEFINITION AR152033
ACCESSION AR152033
VERSION AR152033.1 GI:15118083
KEYWORDS
SOURCE Unknown.
ORGANISM Unknwn.

REFERENCE 1 (bases 1 to 2224)
AUTHORS Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
TITLE TNF ligands
JOURNAL Patent: US 6232446-A 2 15-MAY-2001;
FEATURES Location/Qualifiers
1..2224
source /organism="unknown"

BASE COUNT 435 a 698 c 689 g 402 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2224;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGGACTT 20
|||||
DB 1762 TCACAGAGTCAGGGACTT 1743

RESULT 3
A78517/c A78517 2253 bp DNA linear PAT 19-OCT-1999
LOCUS Sequence 1 from Patent EP0385939.
DEFINITION A78517
ACCESSION A78517
VERSION A78517.1 GI:6090179
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 2253)
AUTHORS Mett,I. and Wallach,D.
TITLE TNF LIGANDS
JOURNAL Patent: EP 0585939-A 1 09-MAR-1994;
YEDA RES & DEV (IL)

FEATURES Location/Qualifiers
1..2253
source /organism="unidentified"

/db_xref="taxon:32644"
90..1475
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB58915.1"
/db_xref="GI:6090180"
translation="MAPVAVMAALAVGLELMAAAHALPAQVAFTYAPEPGSTCLRLRE
YFDQTAQCCSKSPQGHAKVFCTKTSQVCDSDSTYTLWNVWPECLSGSRCS
DKVETQACTREONRITCTCPGWYCALSKQEGCLCAPLRCRPGFVGVARPTETSDVV
CKPAGPTFSTSTSDICRPHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPO
PVYSTRSQHTPTPEPSTAPSTFLLPMGSPPAEGSTGDFALPGLIVGTALGLLII
GVVNCVIMTVQVKKPLCLQREAKVPHLPADKARGTQGPQQHLLITAPSSSSSSLESS
ASALDRRAPTRNPOAPGVEASGAGEARASTGSDSPFGHGTVNVTCIVNVCSDD
HSSQSSQASSTMGDTSDSPSPKDEQVPFSKECAFRSQLETPTLLGSTEEKPLP
LGVPAAGMKPS"

BASE COUNT 440 a 709 c 698 g 406 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2253;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGGACTT 20
|||||
DB 1762 TCACAGAGTCAGGGACTT 1743

RESULT 4
HUMTNFR1I/c HUMTNFR1I 2394 bp mRNA linear PRI 03-SEP-1994
LOCUS Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete
DEFINITION cds.
ACCESSION M55994 M38549
VERSION M55994.1 GI:339757
KEYWORDS glycoprotein; nerve growth factor receptor related; transmembrane
protein; tumor necrosis factor receptor; tumor necrosis factor
receptor II.

SOURCE Homo histiocytic lymphoma cell line U937, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2394)
Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W.,
Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.

REFERENCE A second tumor necrosis factor receptor gene product can shed a

JOURNAL naturally occurring tumor necrosis factor inhibitor
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)
PUBMED 91045991
FEATURES 2172983

source Location/Qualifiers
1..2394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/cell_type="histiocytic lymphoma"
1..2394
/gene="TNFR11"
93..1478
/gene="TNFR11"
/note="603..611 and 669..677 glycosylation site; 861..947 transmembrane domain; 948..1478 cytoplasmic domain; 159..860 extracellular domain"
/codon_start=1
/evidence=experimental
/product="tumor necrosis factor receptor"
/protein_id="AAA36755.1"
/db_xref="GI:339758"
/translation="MAPVAVMAALAVGLELWAAHALPAQVATPYAPEPGSTCLRLE
YDQTAQCCSKSPGQHAQVCTKTSYDTCDESDSTYTLQNMWPECLSCGRSS
DQVETQACTREONRITCTCRPGWICALSKQECRLCAPLRKCRPGFVGARPGTSDV
CKCAPGTFSTNTSTDCIRPHQICNVVAIPGNASDAVCTSTPTKSNAPGAVHLPP
PVSTRSQHTPTPEPTAPSTFLPMGPPSPAGSTGDFALPGLVIGVTALGLLII
GVNVCVIMTVKKKPLCLQREAKVPHLPADKARTGQPEQHLLITAPSSSSSSLESS
ASALDRAPTRNPOAPGVEASGAGEARASTGSSDSPGGHGTQVNVTCIVNVCSSD
HSSQCSQASSTMGDTDSPPSPKDEQVPSKECAFRSQLETPTLLLGSTEERKPLP
LGVPDAGMKPS"
93..158
/gene="TNFR11"
/note="putative"
159..1475
/gene="TNFR11"
/product="tumor necrosis factor receptor"
/note="putative"

sig_peptide 484 a 743 c 739 g 428 t
mat_peptide 484 a 743 c 739 g 428 t

BASE COUNT 484 a 743 c 739 g 428 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 2394;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGTCAGGACTT 20
|||||
Db 1765 TCACAGAGTCAGGACTT 1746

RESULT 5
HSTNFR2S10/c HSTNFR2S10 2613 bp DNA linear PRI 31-JUL-1996
LOCUS Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 10 and
DEFINITION complete cds.
VERSION U52165
KEYWORDS U52165.1 GI:1469539
SEGMENT 10 of 10
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2613)
REFERENCE
AUTHORS Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
Lepaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and
Brodeur,G.M.
Physical mapping and genomic structure of the human TNFR2 gene
Genomics 35 (1), 94-100 (1996)
MEDLINE 96299745
PUBMED 8661109
REFERENCE 2 (bases 1 to 2613)
AUTHORS Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,

LePaslier,D., Stallard,B.J., Goeddel,D.V., deSauvage,F.J. and
Brodeur,G.M.
Direct Submission
Submitted (25-MAR-1996) Christian P. Beltinger, Division of
Oncology, ARC Rm. 902 D, Children's Hospital of Philadelphia, 324
South 34th Street, Philadelphia, PA 19104-4318, USA
FEATURES Location/Qualifiers
1..2613
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="1p36.2"
join(U52156.1:1..167,U52157.1:1..106,U52158.1:114..242,
U52159.1:17..156,U52160.1:17..100,U52161.1:95..330,
U52162.1:83..160,U52163.1:7..41,U52164.1:7..211,125..2613)
/product="tumor necrosis factor receptor"
join(U52156.1:90..167,U52157.1:7..106,U52158.1:114..242,
U52159.1:17..156,U52160.1:7..100,U52161.1:95..330,
U52162.1:83..160,U52163.1:7..41,U52164.1:7..211,125..405)
/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAC50622.1"
/db_xref="GI:1469541"
/translation="MAPVAVMAALAVGLELWAAHALPAQVATPYAPEPGSTCLRLE
YDQTAQCCSKSPGQHAQVCTKTSYDTCDESDSTYTLQNMWPECLSCGRSS
DQVETQACTREONRITCTCRPGWICALSKQECRLCAPLRKCRPGFVGARPGTSDV
CKCAPGTFSTNTSTDCIRPHQICNVVAIPGNASDAVCTSTPTKSNAPGAVHLPP
PVSTRSQHTPTPEPTAPSTFLPMGPPSPAGSTGDFALPGLVIGVTALGLLII
GVNVCVIMTVKKKPLCLQREAKVPHLPADKARTGQPEQHLLITAPSSSSSSLESS
ASALDRAPTRNPOAPGVEASGAGEARASTGSSDSPGGHGTQVNVTCIVNVCSSD
HSSQCSQASSTMGDTDSPPSPKDEQVPSKECAFRSQLETPTLLLGSTEERKPLP
LGVPDAGMKPS"
join(U52157.1:7..112,U52158.1:1..248,U52159.1:1..200,
U52160.1:1..106,U52161.1:1..336,U52162.1:1..218,
U52163.1:1..58,U52164.1:1..234,1..2613)
/gene="TNFR2"
1..124
/gene="TNFR2"
/number=9
125..2613
/gene="TNFR2"
/number=10
BASE COUNT 553 a 750 c 742 g 568 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2613;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGTCAGGACTT 20
|||||
Db 692 TCACAGAGTCAGGACTT 673

RESULT 6
G26865/c human STS SHGC-31494, sequence tagged site.
LOCUS G26865
DEFINITION STS: STS sequence; primer; sequence tagged site.
VERSION G26865.1 GI:1375115
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3380)
REFERENCE
AUTHORS Myers,R.M.
JOURNAL Unpublished (1995)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA

Tel: 4157259687
Fax: 4157259689
Email: myerseshc.stanford.edu

Primer A: CCCACACTAGGACTCTGA
Primer B: CACAGAGACTCAGGACTTGC
STS size: 201
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from M23215
-- Washington University/Merck EST sequence.

FEATURES

source
1. .3380
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="1"
STS
primer_bind 1561..1761
primer_bind 1561..1580
complement(1741..1761)
BASE COUNT 703 a 1029 c 1004 g 644 t
ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 3380;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGACTCAGGACTT 20
|||||

Db 1762 TCACAGAGACTCAGGACTT 1743

RESULT 7

S63368/c
LOCUS S63368 3492 bp mRNA linear PRI 06-MAR-2001
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, partial cds.
ACCESSION S63368
VERSION S63368.1 GI:235648
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3492)
TITLE Dembic, Z., Loetscher, H., Gubler, U., Pan, Y. C., Lahm, H. W., Gentz, R.,
Brockhaus, M. and Lesslauer, W.
Two human TNF receptors have similar extracellular, but distinct
intracellular, domain sequences

JOURNAL Cytokine 2 (4), 231-237 (1990)
MEDLINE 91370690
PubMed 1966549
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 63368] from the original journal article.
This sequence comes from Figure 1.

FEATURES

Location/Qualifiers

source

1. .3492
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS
<1..1278
/note="75-kda; This sequence comes from Figure 1; TNF
receptor"

/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAB19824.2"
/db_xref="GI:13236879"
/translation="GSTCRLREYDQTQACMCCSKGPGQHAKVFCTKTSDTVCDSCED
STYTOLMNMVPECLSGSRCSDDVQACTREONRICTCRPGHYCALSKOEGRLCA
PLURKCRPGVARGPCTETSDVCKPCAPCTESNTTSTDICRPHQICNVVAIPGNASM
DAVCTSTPTSRMAPGAVHLPOPVSTRSQHTQPTPEPSTAPSTFLLPMGSPPAEGS
TCDFALPVGLIVGTALGLLIIGVNVCKKPLCLQREAKVPHLPADKARGTQ
GPEQHLITAPSSSSSSLESSALSALDRRAPTRNOQAPGEASGAGARASTSSDS
SPGHHGTQNVNVCIVNVCSSSDSHSQSASSTNGDTSSPSPKDEQVPFDSKEEC
AFRSQLETPELTLGSTEKPLPLGVPDAGMKPS"

BASE COUNT 757 a 1031 c 1006 g 698 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 3492;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGACTCAGGACTT 20
|||||

Db 1565 TCACAGAGACTCAGGACTT 1546

RESULT 8

AX333705/c
LOCUS AX333705 3683 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 4214 from Patent WO0194629.
ACCESSION AX333705
VERSION AX333705.1 GI:18124424
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE Young, P. E., Augustus, M., Carter, K. C., Ebner, R. R., Endress, G.,
Horrihan, S., Soppet, D. R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets

JOURNAL Patent: WO 0194629-A 4214 13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES

source
1. .3683
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 781 a 1098 c 1086 g 718 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGACTCAGGACTT 20
|||||

Db 1762 TCACAGAGACTCAGGACTT 1743

RESULT 9

AX348016/c
LOCUS AX348016 3683 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 49 from Patent EP1172444.
ACCESSION AX348016
VERSION AX348016.1 GI:18614126
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber, S., Hampe, J. and Mascheretti, S.
Diagnostic use of polymorphisms in the gene coding for the tnfr receptor II and method for detecting non-responders to anti-tnf therapy
Patent: EP 1172444-A 49 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
1..3683
/organism="Homo sapiens"
/db_xref="taxon:9606"
90..1475
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22795.1"
/db_xref="GI:18614127"
/translation="MAPVAVMAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLRE YYDQTAMCCSKSPGQHKAFCTKTSDTVCDSCEDSTYTQLWNWVPECLSGRCSS DQVETQACTREQNRICTRPGWYCALSKQEGRLCAPLRKCRPGFVARPGTETSDVY CKPCAPGTFSTNTSTDICRPHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ PVSTRSQHTOPTPEPSTAPSTSFLLPMGPPPAEGSTGDFALPVLGVLTALGLLII GYVNCVIMTVQVKKKPLCLQREAKVPHLPADKARGTGQPEQOHLITAPSSSSSSLESS ASALDRRAPTRNOPQAPGVEASGAGEARASTGSSSPGGHGTQVNVTCIYNVCSSSD HSSQCSQASSTMGDTDSSPESPKDEQVFPFKECAFRSQLETPTLLGSTEEKPLP LGVPDAGMKPS"
156
mat_peptide 781 a 1098 c 1086 g 718 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
|||||
Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 10
AX348018/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
CDS

AX348018
Sequence 51 from Patent EP1172444.
AX348018
Version
GI:18614128
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber, S., Hampe, J. and Mascheretti, S.
Diagnostic use of polymorphisms in the gene coding for the tnfr receptor II and method for detecting non-responders to anti-tnf therapy
Patent: EP 1172444-A 51 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
1..3683
/organism="Homo sapiens"
/db_xref="taxon:9606"
90..1475
/note="unnamed protein product"
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156
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BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
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Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 10
AX348018/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
CDS

AX348018
Sequence 51 from Patent EP1172444.
AX348018
Version
GI:18614128
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber, S., Hampe, J. and Mascheretti, S.
Diagnostic use of polymorphisms in the gene coding for the tnfr receptor II and method for detecting non-responders to anti-tnf therapy
Patent: EP 1172444-A 51 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 12
HUMAN/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

HUMAN
Human tumor necrosis factor receptor mRNA, complete cds.
M32315
M32315.1
GI:189185
c-myc proto-oncogene; necrosis factor receptor.
Homo sapiens lung cDNA to mRNA.

ASALDRRAPTRNOPQAPGVEASGAGEARASTGSSSPGGHGTQVNVTCIYNVCSSSD HSSQCSQASSTMGDTDSSPESPKDEQVFPFKECAFRSQLETPTLLGSTEEKPLP LGVPDAGMKPS"
156
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BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 11
AX348020/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
CDS

AX348020
Sequence 53 from Patent EP1172444.
AX348020
Version
GI:18614130
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber, S., Hampe, J. and Mascheretti, S.
Diagnostic use of polymorphisms in the gene coding for the tnfr receptor II and method for detecting non-responders to anti-tnf therapy
Patent: EP 1172444-A 53 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
1..3683
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90..1475
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BASE COUNT
ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
|||||
Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 12
HUMAN/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

HUMAN
Human tumor necrosis factor receptor mRNA, complete cds.
M32315
M32315.1
GI:189185
c-myc proto-oncogene; necrosis factor receptor.
Homo sapiens lung cDNA to mRNA.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3683)
AUTHORS Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P.,
Jerzy,R., Dower,S.K., Cosman,D. and Goodwin,R.G.
TITLE A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins
JOURNAL Science 248 (4958), 1019-1023 (1990)
MEDLINE 90260639
PUBMED 2160731
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by C.A.Smith, 30-MAR-1990, for release after publication.
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BASE COUNT 781 a 1098 c 1086 g 718 t
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Best local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCACAGAGACTCAGGACTT 20
|||||
Db 1762 TCACAGAGACTCAGGACTT 1743
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LOCUS HS1118D24
DEFINITION Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33.
Contains part of a novel gene similar to worm genes T08G11.1 and
C25H3.9, part of a 60S Ribosomal Protein L10 LiKE (pseudo)gene and
two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2
(75 kd) (TNF Binding Protein 2, TBPI1, TNF-R2, CD120B, TNFR).
Contains ESTs, STSS, GSSs, genomic marker D1S434 and a ca repeat
polymorphism, complete sequence.
ACCESSION AL031276
VERSION AL031276.1 GI:3947780
KEYWORDS HTG; 60S Ribosomal Protein L10; C25H3.9; ca repeat polymorphism;
CD120B; D1S434; T08G11.1; TBPI1; TNF Binding Protein 2; TNF-R2;
TNFR2; TNFR2; Tumor Necrosis Factor Receptor 2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 115602)
AUTHORS Heath,P.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT requests: clonerequest@sanger.ac.uk
On Dec 2, 1998 this sequence version replaced gi:3724207.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 1118D24. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre Chromosome 1
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
1118D24 is from the library RPC15 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/ VECTOR: pcypac2.
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repeat_region 963..1520
prim_transcript 1677..1797
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repeat_region 1824..2133
/note="MIR repeat: matches 51..176 of consensus"
repeat_region 2152..2413
/note="AluSg repeat: matches 5..310 of consensus"
repeat_region 2418..2569
/note="AluSc repeat: matches 46..307 of consensus"
repeat_region 2671..2966
/note="L2 repeat: matches 2578..2749 of consensus"
repeat_region 3591..3823
/note="AluX repeat: matches 1..297 of consensus"
repeat_region 3824..4120
/note="L2 repeat: matches 1985..2218 of consensus"
repeat_region 4121..4505
/note="AluSc repeat: matches 1..299 of consensus"
repeat_region 4637..4916
/note="L2 repeat: matches 2218..2731 of consensus"


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/note="MIR repeat: matches 2. .155 of consensus"
repeat_region 5385. .5643
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repeat_region 5644. .5726
/note="MIR repeat: matches 155. .234 of consensus"
repeat_region 6026. .6347
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prim_transcript 8059. .8580
/note="match: EST AA489193"
repeat_region 9367. .9716
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repeat_region 9717. .10429
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repeat_region 10473. .10537
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repeat_region 10870. .11006
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repeat_region 11007. .11107
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repeat_region 11108. .11417
/note="AluX repeat: matches 1. .310 of consensus"
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repeat_region 11496. .11569
/note="MER21B repeat: matches 257. .335 of consensus"
repeat_region 11570. .11703
/note="L1PA16 repeat: matches 6000. .6157 of consensus"
repeat_region 12508. .12917
/note="L1M4 repeat: matches 2762. .3194 of consensus"
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repeat_region 13368. .13502
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repeat_region 13752. .13927
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repeat_region 16795. .17083
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repeat_region 18823. .18676
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repeat_region 24136. .24225
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/note="L1MC5 repeat: matches 7260. .7577 of consensus"
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repeat_region 29978. .30692
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGATCAGGACTT 20
|||||
Db 104308 TCACAGAGATCAGGACTT 104327

RESULT 14
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DEFINITION Homo sapiens chromosome 1 clone RP5-1125M11, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION AL355998
VERSION AL355998.9 GI:15523662
KEYWORDS HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 122105)
AUTHORS Smith,M.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 7, 2001 this sequence version replaced gi:13897067.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ1125M11
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----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 121044 bases at least Q40
Consensus quality: 121310 bases at least Q30
Consensus quality: 121451 bases at least Q20
Insert size: 122105; sum-of-contigs
Insert size: 142339; 6.8% error; agarose-fp
Quality coverage: 8.74x in Q20 bases; sum-of-contigs Quality
coverage: 7.58x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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BASE COUNT 27894 a 31136 c 32658 g 30417 t
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION Homo sapiens chromosome 1 clone RP11-353D18 map 1, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
AC023251
AC023251.3 GI:8076833
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
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Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,A., Tirigilio,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo.A., Wu.X., Wyman,D., Ye.W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-FEB-2000) Whitehead Institute/MIT Center for Genome

```

REFERENCE
AUTHORS

Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 187877)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
 Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
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 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye.W.J.,
 Young,G., Zalnoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 25, 2000 this sequence version replaced gi:7139786.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L6342
 Center clone name: 353_D_18
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 177330 bases at least Q40
 Consensus quality: 182502 bases at least Q30
 Consensus quality: 184382 bases at least Q20
 Insert size: 188000; agarose-fp
 Insert size: 185477; sum-of-contigs
 Quality coverage: 4.9 in Q20 bases; agarose-fp
 Quality coverage: 4.9 in Q20 bases; sum-of-contigs

TITLE
JOURNAL
COMMENT

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 25 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1587: contig of 1587 bp in length
 * 1588 1687: gap of 100 bp
 * 1688 3808: contig of 2121 bp in length
 * 3809 3908: gap of 100 bp
 * 3909 6391: contig of 2483 bp in length
 * 6392 6491: gap of 100 bp
 * 6492 8438: contig of 1947 bp in length
 * 8439 8538: gap of 100 bp
 * 8539 11095: contig of 2557 bp in length
 * 11096 11195: gap of 100 bp
 * 11196 14256: contig of 3061 bp in length
 * 14257 14356: gap of 100 bp
 * 14357 18925: contig of 4569 bp in length
 * 18926 19025: gap of 100 bp
 * 19026 22429: contig of 3404 bp in length

TITLE
JOURNAL

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* 22430 22529: gap of 100 bp
* 22530 27710: contig of 5181 bp in length
* 27711 27810: gap of 100 bp
* 27811 33955: contig of 6145 bp in length
* 33956 34055: gap of 100 bp
* 34056 39058: contig of 5003 bp in length
* 39059 39158: gap of 100 bp
* 39159 44172: contig of 5014 bp in length
* 44173 44272: gap of 100 bp
* 44273 50808: contig of 6536 bp in length
* 50809 50908: gap of 100 bp
* 50909 57062: contig of 6154 bp in length
* 57063 57162: gap of 100 bp
* 57163 64064: contig of 6902 bp in length
* 64065 64164: gap of 100 bp
* 64165 70384: contig of 6220 bp in length
* 70385 70484: gap of 100 bp
* 70485 77931: contig of 7447 bp in length
* 77932 78031: gap of 100 bp
* 78032 85239: contig of 7208 bp in length
* 85240 85339: gap of 100 bp
* 85340 93719: contig of 8380 bp in length
* 93720 93819: gap of 100 bp
* 93820 102274: contig of 8455 bp in length
* 102275 102374: gap of 100 bp
* 102375 113890: contig of 11516 bp in length
* 113891 113990: gap of 100 bp
* 113991 124382: contig of 10392 bp in length
* 124383 124482: gap of 100 bp
* 124483 138011: contig of 13529 bp in length
* 138012 138111: gap of 100 bp
* 138112 154313: contig of 16202 bp in length
* 154314 154413: gap of 100 bp
* 154414 187877: contig of 33464 bp in length.

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGACTCAGGACTT 20
|||||
Db 144611 TCACAGAGAGTTCAGGACTT 144592

Search completed: December 6, 2002, 03:57:24
Job time : 170.647 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 4.80891 Seconds
(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937A-5

Perfect score: 20

Sequence: 1 tcacagagagtcaggagactt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	21 AAA49211	Human tumour necro
C 2	20	100.0	2224	16 AA089544	p75 Tumour Necrosi
C 3	20	100.0	2393	12 AAQ10907	40kD TNF inhibitor
C 4	20	100.0	2394	22 AAC83951	Human 40 kDa TNF i
C 5	20	100.0	2613	21 AAA49207	Human tumour necro
C 6	20	100.0	3683	24 ABK83997	Human cDNA differe
C 7	20	100.0	3683	24 ABL65877	Lung cancer relate
C 8	20	100.0	3683	24 ABK33465	Human TNF receptor
C 9	20	100.0	3683	24 ABK33466	Human TNF receptor

C 10	20	100.0	3683	24	ABK33467	Human TNF receptor
C 11	19	95.0	21	24	ABL43100	Human chromosome 1
C 12	19	95.0	201	19	AAQ12093	Human biallelic po
C 13	18.4	92.0	2339	12	AAQ10956	Encodes human 75kD
C 14	18.4	92.0	2339	20	AAQ09171	Human tumour necro
C 15	18.4	92.0	2339	22	AAH48860	Human TNFBP-associ
C 16	16.8	84.0	22870	22	AAS41989	Genomic sequence #
C 17	16.8	84.0	22870	22	AAS42010	Genomic sequence #
C 18	16.8	84.0	22870	22	AAK80760	Human immune/haema
C 19	16.8	84.0	22870	22	AAK87148	Human immune/haema
C 20	16.8	84.0	23432	22	AAS35832	Human cardiovascu
C 21	16.8	84.0	220895	24	ABK84798	Human cDNA differe
C 22	16.4	82.0	316	24	ABN76219	Human ORFX polynuc
C 23	16.4	82.0	1699	21	AAC69613	Human secreted pro
C 24	16.4	82.0	167343	24	ABL64403	Stomach cancer rel
C 25	16.4	82.0	167343	24	ABL67239	Thyroid cancer rel
C 26	16	80.0	2779	23	ABL24698	Drosophila melanog
C 27	16	80.0	5136	22	AAH44289	Human spliced tran
C 28	15.8	79.0	60	24	ABN40943	Human secreted pro
C 29	15.8	79.0	285	21	AAC18156	Hepatitis C virus
C 30	15.8	79.0	340	17	AAT27971	Human polynucleoti
C 31	15.8	79.0	344	22	AAI88677	Human nervous syst
C 32	15.8	79.0	546	22	ABA20255	Arabidopsis thalia
C 33	15.8	79.0	1039	21	AAC47150	Human secreted pro
C 34	15.8	79.0	3301	19	AAV34209	Genomic sequence #
C 35	15.8	79.0	6019	23	ABK42832	Barley Mla6-A geno
C 36	15.8	79.0	6793	23	ABL50539	Genomic sequence #
C 37	15.8	79.0	7153	23	ABL50540	Barley Mla6-A geno
C 38	15.8	79.0	9581	22	AAS28461	Genomic sequence #
C 39	15.8	79.0	11234	22	ABA20857	Human nervous syst
C 40	15.8	79.0	107820	22	AAD16230	Human ATP-binding
C 41	15.8	79.0	140036	24	AAS98600	Human genomic DNA
C 42	15.4	77.0	35	21	AA559431	Primer for DNA enc
C 43	15.4	77.0	340	17	AAT27973	Hepatitis C virus
C 44	15.4	77.0	383	21	AAC26586	Human secreted pro
C 45	15.4	77.0	475	21	AAC79720	Human secreted pro

ALIGNMENTS

RESULT 1

AAA49211
ID AAA49211 standard; DNA; 20 BP.

XX AAA49211;

XX 22-NOV-2000 (first entry)

DT Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-8.

DE Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;

XX Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;

KW osteoporosis; PCR primer; ss.

XX Homo sapiens.

XX WO200032826-A1.

XX 08-JUN-2000.

PF 30-NOV-1999; 99WO-US28403.

XX 30-NOV-1998; 98US-0110268.

PR (UYDR-) UNIV DREXEL.

XX Spotila LD;

XX WPI; 2000-412362/35.

XX Identifying individuals at risk of developing osteoporosis comprises

PT assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene

PT in a DNA sample from an individual .

XX PS Example 3; Page 12; 21pp; English.

CC The present sequence is a PCR primer for the three polymorphic sites
CC within exon 10 of the human tumour necrosis factor alpha receptor 2
CC (TNFR2) gene. By determining the genotype of an individual it is possible
CC to identify those at risk of osteoporosis, which is characterised by low
CC bone density and fragile bones, later in life. Those at greatest risk are
CC those who possess allele 1, which is the rarest allele. This is
CC particularly useful as many cases of osteoporosis go undetected at
CC present. The primer can be used to determine an individual's genotype.
CC and, therefore, their risk of osteoporosis.

XX SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGAGTCAGGACTT 20
Dbb 1 TCACAGAGAGTCAGGACTT 20

RESULT 2
AAQ89544/c
ID AAQ89544 standard; DNA; 2224 BP.

XX AC AAQ89544;

XX 31-OCT-1995 (first entry)

XX p75 Tumour Necrosis Factor Receptor.

DE Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
KW receptor; ss...

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 90..1475

FT /*tag= a

FT /product= p75 TNF receptor.

FT misc_difference 1137..1139

FT /*tag= b

FT misc_difference 1140..1142

FT /transl_except= GCA encodes Glycine.

FT /*tag= c

FT misc_difference 1146..1148

FT /transl_except= CCA encodes Alanine.

FT /*tag= d

FT misc_difference 1149..1151

FT /transl_except= GTG encodes Glutamic acid.

FT /*tag= e

FT misc_difference 1152..1154

FT /transl_except= GAG encodes Alanine.

FT /*tag= f

FT misc_difference 1155..1157

FT /transl_except= GCC encodes Arginine.

FT /*tag= g

FT misc_difference 1158..1160

FT /transl_except= AGT encodes Alanine.

FT /*tag= h

FT misc_difference 1161..1163

FT /transl_except= GGG encodes Serine.

FT /*tag= i

FT misc_difference 1167..1169

FT /transl_except= GCC encodes Threonine.

FT /*tag= j

FT misc_difference 1170..1172

FT /transl_except= GAG encodes Serine.

FT /*tag= k

FT misc_difference 1170..1172

FT /transl_except= GCC encodes Serine.

FT misc_difference 1173..1175

FT /*tag= l

FT misc_difference 1176..1178

FT /*tag= m

FT misc_difference 1182..1184

FT /*tag= n

FT misc_difference 1188..1190

FT /*tag= o

FT misc_difference 1191..1193

FT /*tag= p

FT misc_difference 1194..1196

FT /*tag= q

FT misc_difference 1197..1199

FT /*tag= r

FT misc_difference 2000..2002

FT /*tag= s

FT misc_difference 2003..2005

FT /*tag= t

FT misc_difference 2006..2008

FT /*tag= u

FT misc_difference 2012..2014

FT /*tag= v

FT misc_difference 2015..2016

FT /*tag= w

FT misc_difference 2017..2018

FT /*tag= x

FT misc_difference 2019..2021

FT /*tag= y

FT /transl_except= CAG encodes Serine.

EP648783-A.

19-APR-1995.

11-OCT-1994; 94EP-0116015.

12-OCT-1993; 93IL-0107267.

(YEDA) YEDA RES & DEV CO LTD.

(WALL/) WALLACH D.

Beletsky I, Bigda J, Mett I, Wallach D;

WPI; 1995-148673/20.

P-PSDB; AAR72504.

Tumour necrosis factor (TNF) receptor ligand - used to increase
inhibitory effect of a soluble TNF receptor

Disclosure; Figure 2; 18pp; English.

XX A ligand to a member of the tumour necrosis factor (TNF)/nerve
XX growth factor (NGF) receptor family which binds either to the region
XX of the 4th-Cys rich domain of the receptor, or to the region between
XX it and the cell membrane may be used in the production of a
XX pharmaceutical composition for increasing the inhibitory effect of a
XX soluble receptor of the TNF/NGF receptor family. This sequence
XX encodes the p75 TNF receptor. N in the sequence represents an
XX unidentified nucleotide (poor reproduction in specification).

SQ Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other;

Query Match 100.0%; Score 20; DB 16; Length 2224;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGAGTCAGGGACTT 20
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 Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 3
 ID AAQ10907/c
 XX AAQ10907 standard; cDNA; 2393 BP.
 XX AC AAQ10907;
 XX DT 13-MAY-1991 (first entry)
 XX DE 40kD TNF inhibitor precursor gene in c40DK#6.
 XX KW Tumour necrosis factor; inhibitor; ss.
 XX OS Homo sapiens.
 XX PA
 XX FH Key Location/Qualifiers
 XX FT CDS 93..1478
 XX FT /*tag= a
 XX PN AU9058976-A.
 XX PD 24-JAN-1991.
 XX PF 16-JUL-1990; 90AU-0058976.
 XX PR 07-FEB-1990; 90US-0479661.
 XX PR 18-JUL-1989; 89US-0381080.
 XX PR 11-DEC-1989; 89US-0450329.
 XX PA (SYNE-) SYNERGEN INC.
 XX DR WPI; 1991-073847/11.
 XX DR P-PSDB; AAR11001.
 XX PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
 XX PT and -beta, useful as therapeutic agent.
 XX PS Disclosure; Fig 39; 142pp; English.
 XX CC The sequence encodes the entire 40 kD TNF inhibitor. The clone from
 XX CC which the sequence was obt'd. was isolated from a cDNA library
 XX CC prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
 XX CC gene can be inserted into expression vectors for prep'n. of TNF
 XX CC inhibitor for use in the treatment of inflammatory and degenerative
 XX CC diseases.
 XX CC See also AAQ10878, AAQ10884 and AAQ10883.
 XX SQ Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;

Query Match 100.0%; Score 20; DB 12; Length 2393;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGAGTCAGGGACTT 20
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 Db 1764 TCACAGAGAGTCAGGGACTT 1745

RESULT 4
 AAC83951/c
 ID AAC83951 standard; DNA; 2394 BP.
 XX AC AAC83951;

XX DT 02-MAR-2001 (first entry)
 XX DE Human 40 kDa TNF inhibitor precursor coding sequence.
 XX KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
 XX KW 1L-1; inflammatory disease; degenerative disease; human; lymphotoxin; ss.
 XX OS Homo sapiens.
 XX PN US6143866-A.
 XX PD 07-NOV-2000.
 XX PF 19-JAN-1995; 95US-0375242.
 XX PR 19-JUL-1990; 90US-0555274.
 XX PR 09-JUL-1993; 93US-0090366.
 XX PR 18-JUL-1989; 89US-0381080.
 XX PR 11-DEC-1989; 89US-0450329.
 XX PR 07-FEB-1990; 90US-0479661.
 XX PA (AMGE-) AMGEN INC.
 XX PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
 XX PI Vanderslice RW, Vannice J, Kohno T;
 XX DR WPI; 2001-006443/01.
 XX DR P-PSDB; AAB37686.
 XX PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
 XX PT non-native cysteine residue cross-linked with polyethylene glycol,
 XX PT useful for treating inflammatory and degenerative diseases mediated by
 XX PT TNF -
 XX PS Example 12; Fig 39; 82pp; English.
 XX CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
 XX CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
 XX CC novel TNF inhibitors of the present invention are useful as therapeutic
 XX CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
 XX CC for treating inflammatory and degenerative diseases mediated by TNF. The
 XX CC present sequence is the coding sequence for the precursor of 40 kDa TNF
 XX CC inhibitor. The 40 kDa TNF inhibitor can inhibit both TNF alpha and beta
 XX CC (lymphotoxin).
 XX SQ Sequence 2394 BP; 484 A; 743 C; 738 G; 428 T; 1 other;

Query Match 100.0%; Score 20; DB 22; Length 2394;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGAGTCAGGGACTT 20
 |||||
 Db 1765 TCACAGAGAGTCAGGGACTT 1746

RESULT 5
 AAA49207/c
 ID AAA49207 standard; DNA; 2613 BP.
 XX AC AAA49207;
 XX DT 22-NOV-2000 (first entry)
 XX DE Human tumour necrosis factor alpha receptor 2 gene exon 10.
 XX KW Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
 XX KW osteoporosis; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers


```
XX PI Schreiber S, Hampe J, Mascheretti S;
XX DR WPI: 2002-156651/21.
XX DR P-PSDB; AAU75172.
XX PT Detecting non-responders to anti-human necrosis factor therapy,
XX PT comprises testing an individual for homozygosity for a single
XX PT nucleotide polymorphism in the gene coding for the tumour necrosis
XX PT factor receptor II -
XX PS Disclosure: Page 23-27; 45pp; English.
XX CC The present invention relates to a method for detecting non-responders
XX CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
XX CC an individual for homozygosity for at least one single nucleotide
XX CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
XX CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
XX CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
XX CC Met196Arg respectively, are also described. The method of the invention
XX CC is useful for detecting non-responders to anti-TNF therapy such as
XX CC infliximab therapy, or therapy of Crohn's disease. The genes containing
XX CC the 2 novel polymorphisms are useful for diagnostic purposes in
XX CC inflammatory, malignant or other chronic diseases. The present sequence
XX CC encodes for human TNF receptor II.
XX SQ Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 9
ABK33466/c
ID ABK33466 standard; DNA; 3683 BP.
XX AC ABK33466;
XX DT 23-APR-2002 (first entry)
XX DE Human TNF receptor II gene with SNP in exon 2.
XX KW Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
XX KW chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
XX KW inflammatory disorder; chronic disease; receptor; gene;
XX KW single nucleotide polymorphism; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 90..1475
XX FT /*tag= a
XX FT /product= "TNF receptor II variant #1"
XX FT 90..155
XX FT /*tag= b
XX FT sig_peptide
XX FT mat_peptide 156..1472
XX FT /*tag= c
XX FT variation replace (257, A)
XX FT /*tag= d
XX FT /standard_name= "Single nucleotide polymorphism"
XX PN EP1172444-A1.
XX PD 16-JAN-2002.
XX XX 10-JUL-2000; 2000EP-0114786.
XX PF 10-JUL-2000; 2000EP-0114786.
XX PR
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XX PA (CONA-) CONARIS RES INST GMBH.
XX PI Schreiber S, Hampe J, Mascheretti S;
XX DR WPI: 2002-156651/21.
XX DR P-PSDB; AAU75173.
XX PT Detecting non-responders to anti-human necrosis factor therapy,
XX PT comprises testing an individual for homozygosity for a single
XX PT nucleotide polymorphism in the gene coding for the tumour necrosis
XX PT factor receptor II -
XX PS Claim 15; Page 29-33; 45pp; English.
XX CC The present invention relates to a method for detecting non-responders
XX CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
XX CC an individual for homozygosity for at least one single nucleotide
XX CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
XX CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
XX CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
XX CC Met196Arg respectively, are also described. The method of the invention
XX CC is useful for detecting non-responders to anti-TNF therapy such as
XX CC infliximab therapy, or therapy of Crohn's disease. The genes containing
XX CC the 2 novel polymorphisms are useful for diagnostic purposes in
XX CC inflammatory, malignant or other chronic diseases. The present sequence
XX CC represents the human TNF receptor II gene containing the SNP in exon 2.
XX SQ Sequence 3683 BP; 780 A; 1098 C; 1087 G; 718 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 10
ABK33467/c
ID ABK33467 standard; DNA; 3683 BP.
XX AC ABK33467;
XX DT 23-APR-2002 (first entry)
XX DE Human TNF receptor II gene with SNP in exon 6.
XX KW Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
XX KW chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
XX KW inflammatory disorder; chronic disease; receptor; gene;
XX KW single nucleotide polymorphism; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 90..1475
XX FT /*tag= a
XX FT /product= "TNF receptor II variant #2"
XX FT 90..155
XX FT /*tag= b
XX FT sig_peptide
XX FT mat_peptide 156..1472
XX FT /*tag= c
XX FT variation replace (676, T)
XX FT /*tag= d
XX PN EP1172444-A1.
XX PD 16-JAN-2002.
XX XX 10-JUL-2000; 2000EP-0114786.
XX PF
```

```

XX 10-JUL-2000; 2000EP-0114786.
PR (CONA-) CONARIS RES INST GMBH.
PA Schreiber S, Hampe J, Mascheretti S;
XX WPI: 2002-156651/21.
DR P-PSDB; AAU75174.
XX
PT Detecting non-responders to anti-human necrosis factor therapy,
PT comprises testing an individual for homozygosity for a single
PT nucleotide polymorphism in the gene coding for the tumour necrosis
PT factor receptor II
XX
PS Claim 16; Page 35-39; 45pp; English.
XX
CC The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC Met196Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC infliximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC represents the human TNF receptor II gene containing the SNP in exon 6.
XX
SQ Sequence 3683 BP; 780 A; 1098 C; 1088 G; 717 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 11
ABL43100
ID ABL43100 standard; DNA; 21 BP.
XX
AC ABL43100;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:144.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
KW genome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-0068285.
XX
PR 10-MAR-2000; 2000JP-0066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI: 2002-144136/19.
XX
PT Arraying genome clones
XX
PS Claim 4; Page 7; 528pp; Japanese.
XX

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```

CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention.
XX
SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 other;

Query Match 95.0%; Score 19; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACAGAGAGTCAGGGACTT 20
Db 1 CACAGAGAGTCAGGGACTT 19

RESULT 12
AAX12093/c
ID AAX12093 standard; DNA; 201 BP.
XX
AC AAX12093;
XX
DT 30-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic DNA fragment M32315b.
XX
KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
KW treatment; marker; ss.
XX
OS Homo sapiens.
XX
PN WO9820165-A2.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US20313.
XX
PR 06-NOV-1996; 96US-0030455.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Hudson T, Lander ES, Wang D;
XX
DR WPI: 1998-286974/25.
XX
PT New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease
XX
PS Claim 1; Page 219; 310pp; English.
XX
CC AAX10269-X12937 are human DNA fragments which contain biallelic
CC polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site

```

CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
 CC can be used in methods for determining polymorphic forms in an individual
 CC for use in e.g. forensics, paternity testing or for phenotypic typing for
 CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
 CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
 CC familial hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases.

XX
 SQ Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

Query Match 95.0%; Score 19; DB 19; Length 201;

Best Local Similarity 100.0%; Pred. No. 6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CACAGACAGTCAGGACTT 20
 Db 201 CACAGACAGTCAGGACTT 183
 |||||

RESULT 13
 AAQ10956/c
 ID AAQ10956 standard; DNA; 2339 BP.

XX AC AAQ10956;

XX DT 24-MAY-1991 (first entry)

XX DE Encodes human 75kd TNF-binding protein.

XX KW Tumour Necrosis Factor; binding proteins; septic shock;
 XX autoimmune glomerulonephritis; lymphokine; cytokine.

FH Key Location/Qualifiers
 FT CDS 1..1179
 FT /*tag= a
 FT /product= 75kd TNF-BP

XX EP417563-A.

XX PN 20-MAR-1991.

XX PD 31-AUG-1990; 90EP-0116707.

XX PF 20-APR-1990; 90CH-0001347.

XX PR 12-SEP-1989; 89CH-0003319.

XX PA (HOFF) HOFFMANN-LA ROCHE AG.

XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaeger EJ;

XX WPI: 1991-081851/12.

DR P-PSDB: AAR11605.

XX Insoluble tumour necrosis factor binding proteins - and DNA
 PT encoding them, useful in pharmaceutical prods. and for antibody
 PT prodn.

PS Claim 4; Fig 1; 26pp; German.

XX Partial amino acid sequences were determined for the 55 and 75kd
 CC TNF-BPs (see AAR1072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used

CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gt11. Positive clones were
 CC identified and sequenced. Repeated sequencing showed a discrepancy
 CC at position 7 such that the third codon encodes either Thr or Ser.
 CC DNA constructs comprising the TNF-BP coding sequence may also
 CC contain a fragment encoding a human Ig domain. Recombinant
 CC constructs are used to transform cells to confer improved TNF-
 CC binding properties.
 CC See also AAQ10955.

XX SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other;

Query Match 92.0%; Score 18.4; DB 12; Length 2339;

Best Local Similarity 95.0%; Pred. No. 16;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCACAGACAGTCAGGACTT 20
 Db 1465 TCACAGACAGTCAGGACTT 1446
 |||||

RESULT 14

AAZ09171/c

ID AAZ09171 standard; cDNA; 2339 BP.

XX AC AAZ09171;

XX DT 18-OCT-1999 (first entry)

XX DE Human tumour necrosis factor binding protein cDNA fragment.

XX KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
 KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
 KW autoimmune glomerulonephritis; cerebral malaria; immune response;
 KW antagonist; diagnosis; ds.

XX OS Homo sapiens.

FH Key Location/Qualifiers
 FT CDS 1..1179
 FT /*tag= a
 FT /product= "TNF binding protein"
 FT /note= "Partial sequence, no start codon given"

XX EP939121-A2.

XX PN 01-SEP-1999.

XX PD 31-AUG-1990; 90EP-0116707.

XX PF 20-APR-1990; 90CH-0001347.

XX PR 12-SEP-1989; 89CH-0003319.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
 PI Schlaeger E;

XX WPI: 1999-480840/41.

DR P-PSDB: AAY30935.

XX New insoluble proteins, and fragments, that bind to tumor necrosis
 PT factor, used to treat e.g. septic shock or cerebral malaria

XX Claim 4a; Fig 4; 25pp; German.

XX This invention describes novel homogeneous insoluble proteins (I),
 CC their (in)soluble fragments (Ia) and their salts that can bind tumour
 CC necrosis factor (TNF). The products of the invention have
 CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (I)
 CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
 CC glomerulonephritis, cerebral malaria, immune responses and inflammation),

CC (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence encodes
CC a tumour necrosis factor binding protein fragment described in the method
CC of the invention.

XX
SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;
Query Match 92.0%; Score 18.4; DB 20; Length 2339;
Best Local Similarity 95.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCACAGAGAGTCAGGACTT 20
||||||| |||||||
Db 1465 TCACAGAGACTCAGGACTT 1446

RESULT 15

AAH48860/c
ID AAH48860 standard; DNA: 2339 BP.

XX AC AAH48860;

DT 12-NOV-2001 (first entry)

DE Human TNFBP-associated DNA #2.

XX TNF: Lumor necrosis factor binding protein; TNFBP; treatment;
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 1..1179

FT /*tag= a
FT /product= "TNFBP-associated protein"

XX EP1132471-A2.

XX PD 12-SEP-2001.

XX PF 31-AUG-1990; 2001EP-0108117.

XX PR 12-SEP-1989; 89CH-0003319.

XX PR 08-MAR-1990; 90CH-0000746.

XX PR 20-APR-1990; 90CH-0001347.

XX PR 31-AUG-1990; 90EP-0116707.

XX PR 31-AUG-1990; 99EP-0100703.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

XX Schlaeger E;

DR WPI: 2001-559312/63.

DR P-PSDB: AAB86818.

XX New homogeneous, insoluble proteins that bind tumor necrosis factor
XX (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -

PS Claim 4a: Fig 4; 26pp; German.

XX This invention describes novel insoluble proteins (I), also their
XX (in)soluble fragments and pharmaceutically acceptable salts, able to bind
XX tumor necrosis factor (TNF) and in homogeneous form. The products of the
XX invention have antiinflammatory, immunosuppressive, antibacterial,
XX antiprotozoal activity. (I), and related recombinant proteins, are used
XX to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
XX sepsis; development of autoimmune glomerulonephritis and cerebral
XX malaria. Also (I), or antibodies specific for them, are used for
XX diagnostic determination of TNF in body fluids, for affinity purification

CC of TNF and for identifying (antagonists of TNF. This sequence encodes a
CC human TNF binding protein described in the method of the invention.

XX
SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;
Query Match 92.0%; Score 18.4; DB 22; Length 2339;
Best Local Similarity 95.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCACAGAGAGTCAGGACTT 20
||||||| |||||||
Db 1465 TCACAGAGACTCAGGACTT 1446

Search completed: December 5, 2002, 23:30:10
Job time : 9.80891 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 : Search time 38.2783 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937A-5
Perfect score: 20
Sequence: 1 tcacagagagtcaggactt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estinu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	337	10 AW801622	AW801622 IL5-UM006
C 2	20	100.0	372	9 AA031826	AA031826 zk14b11.r
C 3	20	100.0	384	9 AA353635	AA353635 EST61785
C 4	20	100.0	472	10 AV746487	AV746487 AV746487
5	20	100.0	640	10 BE299702	BE299702 600944393
C 6	20	100.0	655	14 BQ632819	BQ632819 i128d03.y

C 7	20	100.0	974	12 BG745202	BG745202 602723532
C 8	20	100.0	1053	14 BQ052282	BQ052282 AGENCOURT
C 9	20	100.0	1066	12 BF568708	BF568708 602184353
C 10	20	100.0	1102	14 BM917316	BM917316 AGENCOURT
C 11	20	100.0	1183	12 BF569011	BF569011 602184353
C 12	20	100.0	1470	12 BF569050	BF569050 602184408
C 13	20	100.0	2291	11 BC011844	BC011844 Homo sapi
C 14	18	90.0	932	12 BG829828	BG829828 602764119
C 15	17.4	87.0	121	17 BH352650	BH352650 CH230-55A
C 16	17.4	87.0	310	10 BB221242	BB221242 BB221242
C 17	17.4	87.0	450	17 AQ812560	AQ812560 HS-5249_B
C 18	17.4	87.0	623	17 AZ837703	AZ837703 2M0133B08
C 19	17	85.0	391	17 AQ437855	AQ437855 HS_5057_A
C 20	17	85.0	392	9 AI448146	AI448146 mo63d07.x
C 21	17	85.0	452	9 AI262090	AI262090 qz28b12.y
C 22	17	85.0	687	17 AZ983907	AZ983907 2M0265A16
C 23	17	85.0	770	13 BI646518	BI646518 603277607
C 24	16.8	84.0	303	17 AZ915807	AZ915807 RPCI-24-1
C 25	16.8	84.0	332	12 BF857218	BF857218 RC5-PT019
C 26	16.8	84.0	510	17 AQ825259	AQ825259 CITBI-EI-
C 27	16.8	84.0	546	17 AZ887751	AZ887751 RPCI-24-1
C 28	16.8	84.0	572	17 AQ426991	AQ426991 CITBI-EI-
C 29	16.8	84.0	621	17 DR2A23S	DR2A23S DanLo ref
C 30	16.8	84.0	710	10 BB341493	BB341493 BB341493
C 31	16.8	84.0	872	14 BQ730759	BQ730759 AGENCOURT
C 32	16.4	82.0	180	13 BM482728	BM482728 535740_MA
C 33	16.4	82.0	274	10 BB475383	BB475383 BB475383
C 34	16.4	82.0	289	10 BB324937	BB324937 BB324937
C 35	16.4	82.0	308	17 AQ647902	AQ647902 RPC193-Dp
C 36	16.4	82.0	372	14 W40081	W40081 T2594_MVAT4
C 37	16.4	82.0	377	17 AQ637005	AQ637005 RPCI-11-4
C 38	16.4	82.0	449	17 AQ043251	AQ043251 CIT-HSP-2
C 39	16.4	82.0	487	9 AI450485	AI450485 mc34d07.y
C 40	16.4	82.0	494	17 AQ538916	AQ538916 RPCI-11-3
C 41	16.4	82.0	501	17 AQ184218	AQ184218 HS_3223_A
C 42	16.4	82.0	526	17 AQ836108	AQ836108 HS_5524_A
C 43	16.4	82.0	537	17 AQ439298	AQ439298 HS_5060_B
C 44	16.4	82.0	553	10 BE234177	BE234177 140926_MA
C 45	16.4	82.0	570	17 AQ701572	AQ701572 HS_2130_A

ALIGNMENTS

RESULT 1
AW801622
LOCUS
DEFINITION IL5-UM0068-080400-056-b02 UM0068 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW801622
VERSION AW801622.1 GI:7853492
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)

REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

TITLE
JOURNAL
MEDLINE
COMMENT

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=4t2=IL5-UM0068-080
 400-056-b02ct3-2000-04-08&L4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 336.
 Location/Qualifiers

FEATURES

source

1. .337
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UM0068"
 /dev_stage="Adult"
 /note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 90 a 108 c 95 g 44 t

Query Match 100.0%; Score 20; DB 10; Length 337;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGACTCAGGGACTT 20
 |||||

Db 251 TCACAGAGACTCAGGGACTT 270

RESULT 2

AA031826/c

LOCUS

zk14b11.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
 IMAGE:470493 5' similar to gb:M32315 TUMOR NECROSIS FACTOR RECEPTOR
 2 PRECURSOR (HUMAN); contains element PTR5 repetitive element ;
 mRNA sequence.

AA031826.1 GI:1501789

EST.

SOURCE

human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 372)
 Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
 ,B., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N., Mardis,E., Moore
 ,B., Morris,M., Parsons,J.B., Prange,C., Rifkin,L., Rohlfing,T.,
 Schellenberg,K., Soares,M.B., Tan,F., Thierry-Neg J., Trevaskis,E.,
 Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 849 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 362.

Location/Qualifiers

1. .372

/organism="Homo sapiens"

/db_xref="GDB:3756495"

/db_xref="taxon:9606"

/clone="IMAGE:470493"

FEATURES

source

/clone_lib="Soares_pregnant_uterus_NbHPU"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(OT) primer [5'
 AACGGAAGAAATTCGGCGCCCTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."
 51 a 122 c 102 g 97 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 372;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGACTCAGGGACTT 20

|||||

Db 230 TCACAGAGACTCAGGGACTT 211

|||||

RESULT 3

AA353635/c

LOCUS

EST61785 Activated T-cells XX Homo sapiens cDNA 5' end similar to
 tumor necrosis factor receptor 2, mRNA sequence.
 AA353635
 AA353635.1 GI:2005955
 EST.

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 384)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
 ,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White
 ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Claydon,R.A.,
 Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
 ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodok,A.,
 Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
 Kelley,J.C., Liu,L.I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
 Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
 Kunsch,C., HungJun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
 Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
 ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
 Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)

TITLE

JOURNAL

MEDLINE

COMMENT

Other_ESTs: THCI66535

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M3 Reverse.

Location/Qualifiers

1. .384

FEATURES

source

LOCUS	BE299702	640 bp	mRNA	linear	EST 20-JUL-2002							
DEFINITION	600944393T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960374 3', mRNA sequence.											
ACCESSION	BE299702											
VERSION	BE299702.1	GI:9183450										
KEYWORDS	EST.											
SOURCE	human.											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
AUTHORS	NIH-MGC 1 to 640)											
TITLE	NIH-MGC http://mgc.nci.nih.gov/.											
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)											
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM53 row: j column: 23 High quality sequence start: 69 High quality sequence stop: 638. Location/Qualifiers 1..640											
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BASE COUNT	141 a 203 c 174 g 122 t											
ORIGIN												
Query Match	100.0%; Score 20; DB 10; Length 640;											
Best Local Similarity	100.0%; Pred. No. 66;											
Matches	20; Conservative	0; Mismatches	0; Indels	0; Gaps	0;							
QY	1	TCACAGACAGTCAGGGACTT	20									
Db	582	TCACAGACAGTCAGGGACTT	601									
RESULT 6												
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DEFINITION	B0632819 i128d03.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6031157 5', mRNA sequence.											
ACCESSION	B0632819											
VERSION	B0632819.1	GI:21684337										
KEYWORDS	EST.											
SOURCE	human.											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
AUTHORS	1 (bases 1 to 655)											
	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Prestell,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising-B., Ritter,E., Ronko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.											
TITLE	Endocrine Pancreas Consortium											

FEATURES


```

Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGGACTT 20
|||||
Db 633 TCACAGAGAGTCAGGGACTT 652

RESULT 9
BF568708/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1159 row: 1 column: 13
High quality sequence stop: 712.
FEATURES
source
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4300500"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH_MGC Library. |"
BASE COUNT 216 a 316 c 354 g 180 t
ORIGIN
Query Match 100.0%; Score 20; DB 12; Length 1066;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGGACTT 20
|||||
Db 671 TCACAGAGAGTCAGGGACTT 652

RESULT 10
BM917316/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1102 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6606593 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483819
5', mRNA sequence.
BM917316
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1183)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1159 row: 1 column: 13
High quality sequence stop: 716.

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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1102)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2012 row: b column: 12
High quality sequence stop: 507.
FEATURES
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Location/Qualifiers
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/clone="IMAGE:5483819"
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/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 219 a 366 c 292 g 222 t 3 others
ORIGIN
Query Match 100.0%; Score 20; DB 14; Length 1102;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGGACTT 20
|||||
Db 284 TCACAGAGAGTCAGGGACTT 265

RESULT 11
BF569011
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1183 bp mRNA linear EST 12-DEC-2000
602184333T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 3',
mRNA sequence.
BF569011
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1183)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1159 row: 1 column: 13
High quality sequence stop: 716.

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FEATURES

source

Location/Qualifiers
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/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
308 a 357 c 348 g 170 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 1183;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGACTCAGGACTT 20

|||||
Db 555 TCACAGAGACTCAGGACTT 574

RESULT 12

BF569050

LOCUS

DEFINITION 602184408T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300633 3',
mRNA sequence.

ACCESSION BF569050

VERSION 1 GI:11642430

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1470)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM1159 row: 0 column: 02

High quality sequence stop: 710.

FEATURES

source

Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

BASE COUNT
ORIGIN

454 a 454 c 367 g 195 t

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 1470;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGACTCAGGACTT 20

|||||

Db 559 TCACAGAGACTCAGGACTT 578

RESULT 13

BC011844/c

LOCUS

DEFINITION BC011844 Homo sapiens, Similar to tumor necrosis factor receptor
superfamily, member 1B, clone IMAGE:4111730, mRNA.

ACCESSION BC011844

VERSION 1 GI:15080140

KEYWORDS HTC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2291)

Strausberg, R.

Direct Submission

Submitted (30-JUL-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov

Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G., Brinkley, C., Brooks, S.,

Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,

Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,

Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,

Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRAL Plate: 28 Row: 1 Column: 15

This clone was selected for full length sequencing because it

passed the following selection criteria: Similarity but not

identity to protein

This clone has the following problem: incomplete processing.

FEATURES

source

Location/Qualifiers
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/lab_host="DH10B-R"
/note="Vector: pOTB7"

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ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCACAGAGACTCAGGACTT 20
|||||
Db 1671 TCACAGAGACTCAGGACTT 1652

RESULT 14
BG829828/c
LOCUS
DEFINITION 932 bp mRNA linear EST 22-MAY-2001
602764119F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899436 5',
mRNA sequence.
ACCESSION BG829828
VERSION BG829828.1 GI:14177415
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arranged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1791 row: e column: 05
High quality sequence stop: 833.

FEATURES
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/lab_host="DH10B (phage-resistant)"
/note="organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
BASE COUNT 162 a 296 c 296 g 177 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ACAGAGACTCAGGACTT 20
|||||
Db 782 ACAGAGACTCAGGACTT 765

RESULT 15
BH352650/c
LOCUS
DEFINITION 121 bp DNA linear GSS 03-DEC-2001
CH230-55A15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-55A15, DNA sequence.
ACCESSION BH352650
VERSION BH352650.1 GI:17283384
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.
1 (bases 1 to 121)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-55A15.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 55 row: A column: 15
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..121
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT 32 a 30 c 29 g 30 t
ORIGIN
Query Match 87.0%; Score 17.4; DB 17; Length 121;
Best Local Similarity 94.7%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CACAGAGTCAGGACTT 20
|||||
Db 41 CACAGAGTCAGGACTT 23

Search completed: December 6, 2002, 04:54:42
Job time : 50.2783 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 ; Search time 1.03896 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-5

Perfect score: 20

Sequence: 1 tcacagagagtcaggagctt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_NA:*
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
 - 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
 - 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
 - 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
 - 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2224	4	US-08-477-347-2
C 2	20	100.0	2224	4	US-08-476-862-1
C 3	20	100.0	3683	4	US-09-844-634-3
C 4	20	100.0	15602	4	US-09-844-634-17
5	15.8	79.0	340	4	US-08-836-075A-69
6	15.4	77.0	35	4	US-09-502-653-51
7	15.4	77.0	340	4	US-08-836-075A-73
8	15.4	77.0	660	4	US-09-221-017B-116
9	15.4	77.0	1200	4	US-09-502-653-7
10	15.2	76.0	15936	4	US-09-147-119-1
11	14.8	74.0	199	3	US-09-058-389A-18
12	14.8	74.0	199	4	US-09-611-781-18
13	14.8	74.0	1489	4	US-09-487-445-10
14	14.8	74.0	2483	2	US-08-177-109A-1
15	14.8	74.0	2483	2	US-08-687-706-1
16	14.8	74.0	6354	3	US-09-058-389A-5
17	14.8	74.0	6354	4	US-09-611-781-5
18	14.8	74.0	45716	4	US-08-965-048-5
19	14.8	74.0	45989	4	US-08-965-048-6
20	14.4	72.0	340	3	US-08-441-971-15
21	14.4	72.0	340	4	US-08-836-075A-71
22	14.4	72.0	340	4	US-08-836-075A-77
23	14.4	72.0	340	4	US-08-836-075A-79
24	14.4	72.0	340	4	US-08-221-653-15
25	14.4	72.0	340	4	US-08-442-144A-15
26	14.4	72.0	340	4	US-08-441-970-15
C 27	14.4	72.0	492	3	US-08-600-430-1

28	14.4	72.0	523	4	US-08-896-164-13	Sequence 13, Appl
C 29	14.4	72.0	648	2	US-08-783-395-4	Sequence 4, Appl
30	14.4	72.0	1739	2	US-08-899-336-1	Sequence 1, Appl
C 31	14.4	72.0	2610	3	US-09-212-771-1	Sequence 1, Appl
C 32	14.4	72.0	2610	3	US-09-091-058-1	Sequence 1, Appl
C 33	14.4	72.0	12537	2	US-08-611-280-4	Sequence 4, Appl
C 34	14.4	72.0	12537	4	US-09-195-940-4	Sequence 4, Appl
C 35	14.4	72.0	12537	4	US-09-562-466-4	Sequence 4, Appl
36	14.2	71.0	319	1	US-08-341-568-5	Sequence 5, Appl
37	14.2	71.0	319	2	US-08-911-020-5	Sequence 5, Appl
38	14.2	71.0	485	4	US-09-085-199B-32	Sequence 32, Appl
39	14.2	71.0	571	4	US-08-991-789A-14	Sequence 14, Appl
40	14.2	71.0	571	4	US-09-062-451-14	Sequence 14, Appl
41	14.2	71.0	571	4	US-09-598-326-14	Sequence 14, Appl
42	14.2	71.0	601	4	US-09-814-951A-7	Sequence 7, Appl
43	14.2	71.0	601	4	US-09-814-951A-8	Sequence 8, Appl
44	14.2	71.0	601	4	US-09-814-951A-9	Sequence 9, Appl
45	14.2	71.0	941	2	US-08-121-436A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-477-347-2/c
; Sequence 2, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

LOCATION: 90..1472
US-08-477-347-2
Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 2
US-08-476-862-1/c
Sequence 1, Application US/08476862
Patent No. 6262239
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472

US-08-476-862-1
Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 3
US-09-844-634-3/c
Sequence 3, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2
FILE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 3
LENGTH: 3683
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)...(1475)
US-09-844-634-3

Query Match 100.0%; Score 20; DB 4; Length 3683;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 4
US-09-844-634-17/c
Sequence 17, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2
FILE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 17
LENGTH: 15602
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-844-634-17

Query Match 100.0%; Score 20; DB 4; Length 15602;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 11295 TCACAGAGAGTCAGGGACTT 11276

RESULT 5
US-08-836-075A-69
Sequence 69, Application US/08836075A
Patent No. 6180768
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

```
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
;
; TITLE OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-836-075A-69

Query Match 79.0%; Score 15.8; DB 4; Length 340;
Best Local Similarity 89.5%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGAGCT 19
|| |||||
Db 294 TCTCAGAGAGTCAGGAGT 312

RESULT 6
US-09-502-653-51
; Sequence 51, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schlein, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sjolholm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481,200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
```

```
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(35)
; OTHER INFORMATION: Primer: Galactanase.B.lich.upper.SacII
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-502-653-51

Query Match 77.0%; Score 15.4; DB 4; Length 35;
Best Local Similarity 94.1%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACAGAGAGTCAGGAC 18
|||||
Db 16 CACAGAGATTCAGGAC 32

RESULT 7
US-08-836-075A-73
; Sequence 73, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-836-075A-73
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Query Match 77.0%; Score 15.4; DB 4; Length 340;
Best Local Similarity 94.1%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCACAGAGTCAGGGA 17
Db 294 TCTCAGAGTCAGGGA 310

RESULT 8

US-09-221-017B-116
; Sequence 116, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: ROSS, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141

INFORMATION FOR SEQ ID NO: 116:

SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...660

Query Match 77.0%; Score 15.4; DB 4; Length 660;
Best Local Similarity 94.1%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCACAGAGTCAGGGA 17
Db 394 TCACAGAGTCAGGGA 410

RESULT 9

US-09-502-653-7
; Sequence 7, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj invad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schleim, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: Stegaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481-200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Bacillus licheniformis ATCC 14580
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1197)
; OTHER INFORMATION: DNA encoding the Galactanase shown in SEQ ID NO.8.
US-09-502-653-7

Query Match 77.0%; Score 15.4; DB 4; Length 1200;
Best Local Similarity 94.1%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CACAGAGTCAGGAC 18
Db 4 CACAGAGTCAGGAC 20

RESULT 10

US-09-147-119-1
; Sequence 1, Application US/09147119
; Patent No. 6338844
; GENERAL INFORMATION:
; APPLICANT: KURTH, Ruth
; APPLICANT: BAIER, Michael
; APPLICANT: BANNERT, No. 6338844bert
; APPLICANT: METZNER, Karin
; APPLICANT: WERNER, Albrecht
; TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, cDNA AND mRNA WHICH
; TITLE OF INVENTION: CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESS FOR THE
; TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,119
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA: PCT/EP97/01753
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA: DE 196 14 099.4
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P1614-8068
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15936 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: exon
LOCATION: 3100..3238
FEATURE:
NAME/KEY: exon
LOCATION: 5540..6635
FEATURE:
NAME/KEY: exon
LOCATION: 7504..7672
FEATURE:
NAME/KEY: exon
LOCATION: 9711..9812
FEATURE:
NAME/KEY: exon
LOCATION: 12065..12323
FEATURE:
NAME/KEY: exon
LOCATION: 12578..12703
FEATURE:
NAME/KEY: exon
LOCATION: 14767..15936
US-09-147-119-1

Query Match 76.0%; Score 15.2; DB 4; Length 15936;
Best Local Similarity 85.0%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
DB 2811 TCATAAGAGTCAGGCTT 2830

RESULT 11
US-09-058-389A-18
Sequence 18, Application US/09058389A
Patent No. 6130065
GENERAL INFORMATION:
APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
TITLE OF INVENTION: A NITROBENZYL MERCAPTOPYRIMIDINE
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058.389A
FILING DATE: April 9, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "intron 8"
HYPOTHETICAL: NO
US-09-058-389A-18

Query Match 74.0%; Score 14.8; DB 3; Length 199;
Best Local Similarity 88.9%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGAC 18
DB 76 TCACAGTGGTCAGGAC 93

RESULT 12
US-09-611-781-18
Sequence 18, Application US/09611781
Patent No. 6423829
GENERAL INFORMATION:
APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
TITLE OF INVENTION: A NITROBENZYL MERCAPTOPYRIMIDINE
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,781
FILING DATE:
CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/058,389
;; FILING DATE: April 9, 1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 1340-1-013N
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-487-5800
;; TELEFAX: 201-343-1684
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 199 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "intron 8"
;; HYPOTHETICAL: NO
;; US-09-611-781-18

Query Match 74.0%; Score 14.8; DB 4; Length 199;
Best Local Similarity 88.9%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCACAGAGAGTCAGGCAC 18
Db 76 TCACAGTGGTCAGGCAC 93
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RESULT 13
US-09-487-445-10
; Sequence 10, Application US/09487445
; Patent No. 6258600
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
; FILE REFERENCE: RTS-0107
; CURRENT APPLICATION NUMBER: US/09/487,445
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 10
; LENGTH: 1489
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(1489)
US-09-487-445-10

Query Match 74.0%; Score 14.8; DB 4; Length 1489;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 ACACAGAGAGTCAGGCATT 20
Db 699 ACAGTGAGTCAGGCATT 716
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RESULT 14
US-08-177-109A-1/c
; Sequence 1, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta

;; STATE: Georgia
;; COUNTRY: USA
;; ZIP: 30309-3450
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/177,109A
;; FILING DATE: 03-JAN-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: WU 107
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 873-8794
;; TELEFAX: (404) 873-8795
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2483 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 116..2407
;; OTHER INFORMATION: /note= "Product = Human Factor B"

US-08-177-109A-1
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Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CACAGAGAGTCAGGCAC 19
Db 1550 CACAGAGACTCAGACT 1533
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RESULT 15
US-08-687-706-1/c
; Sequence 1, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994

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: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: WU 107 DIV
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 873-8794
: TELEFAX: (404) 873-8795
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2483 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 116..2407
: OTHER INFORMATION: /note= "Product = Human Factor B"
US-08-687-706-1

Query Match 74.0%; Score 14.8; DB 2; Length 2483;
Best Local Similarity 88.9%; Pred. No 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CACAGAGAGTCAGGAGCT 19
Db 1550 CACAGAGACTCAGAGACT 1533
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Job time : 12.039 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 20:03:23 : Search time 0.972171 Seconds
(without alignments)
8021.899 Million cell updates/sec

Title: US-09-856-937A-5

Perfect score: 20

Sequence: 1 tcacagagagtcagggaactt 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published-Applications_NA:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2224	10	US-09-800-909-1 Sequence 1, Appl1
C 2	20	100.0	2224	10	US-09-800-908-2 Sequence 2, Appl1
C 3	20	100.0	3683	10	US-09-954-456-1187 Sequence 1187, Ap
C 4	16.8	84.0	23432	10	US-09-764-869-1332 Sequence 1332, Ap
C 5	16.4	82.0	167343	10	US-09-962-436-281 Sequence 281, App
C 6	16.4	82.0	167343	10	US-09-964-824A-273 Sequence 273, App
C 7	15.8	79.0	3301	9	US-09-981-876-66 Sequence 66, Appl
C 8	15.8	79.0	6019	10	US-09-764-847-1719 Sequence 1719, Ap
C 9	15.8	79.0	9581	10	US-09-764-860-895 Sequence 895, App
C 10	15.4	77.0	32204	10	US-09-764-846-306 Sequence 306, App
C 11	15.2	76.0	155	10	US-09-864-761-30451 Sequence 30451, A
C 12	15.2	76.0	285	9	US-09-938-842A-2494 Sequence 2494, Ap
C 13	15.2	76.0	333	10	US-09-867-701-302 Sequence 302, App
C 14	15.2	76.0	406	10	US-09-853-386-31 Sequence 31, Appl
C 15	15.2	76.0	474	10	US-09-864-761-13882 Sequence 13882, A
C 16	15.2	76.0	792	9	US-09-736-457-220 Sequence 220, App
C 17	15.2	76.0	792	9	US-09-902-941-220 Sequence 220, App
C 18	15.2	76.0	807	9	US-09-860-670-58 Sequence 58, Appl
C 19	15.2	76.0	1077	10	US-09-770-445-130 Sequence 130, App

C 20	15	75.0	955	10	US-09-815-248-3 Sequence 3, Appl1
C 21	15	75.0	1066	10	US-09-815-248-1 Sequence 1, Appl1
C 22	14.8	74.0	400	10	US-09-732-561-15 Sequence 15, Appl1
C 23	14.8	74.0	400	10	US-09-887-576-607 Sequence 607, App
C 24	14.8	74.0	446	10	US-09-917-800A-1288 Sequence 1288, Ap
C 25	14.8	74.0	758	10	US-09-822-830A-441 Sequence 441, App
C 26	14.8	74.0	1859	10	US-09-880-192-33 Sequence 33, Appl
C 27	14.8	74.0	2388	10	US-09-880-107-2165 Sequence 2165, Ap
C 28	14.8	74.0	2717	12	US-10-044-090-471 Sequence 471, App
C 29	14.8	74.0	4420	9	US-09-986-234-5 Sequence 5, Appl1
C 30	14.8	74.0	8861	9	US-09-764-868-1445 Sequence 1445, Ap
C 31	14.8	74.0	8861	10	US-09-764-878-412 Sequence 412, App
C 32	14.8	74.0	8887	10	US-09-764-878-412 Sequence 412, App
C 33	14.8	74.0	368004	10	US-09-949-654-3 Sequence 3, Appl1
C 34	14.4	72.0	241	10	US-09-923-876-4906 Sequence 4906, Ap
C 35	14.4	72.0	401	9	US-09-946-807-173 Sequence 173, App
C 36	14.4	72.0	401	10	US-09-795-668-173 Sequence 173, App
C 37	14.4	72.0	401	10	US-09-795-668-173 Sequence 173, App
C 38	14.4	72.0	402	9	US-09-948-807-1388 Sequence 1388, Ap
C 39	14.4	72.0	402	10	US-09-795-668-1388 Sequence 1388, Ap
C 40	14.4	72.0	402	10	US-09-795-668-1388 Sequence 1388, Ap
C 41	14.4	72.0	405	10	US-09-864-761-3630 Sequence 3630, Ap
C 42	14.4	72.0	500	9	US-10-060-841-28 Sequence 28, Appl
C 43	14.4	72.0	523	10	US-09-835-992A-13 Sequence 13, Appl
C 44	14.4	72.0	548	10	US-09-857-701-911 Sequence 911, App
C 45	14.4	72.0	1830	10	US-09-771-161A-41 Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-800-909-1/c
: Sequence 1, Application US/09800909
: Patent No. US20010019833A1
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BIGDA, Jacek
: APPLICANT: BELETSEY, Igor
: APPLICANT: METT, Igor
: APPLICANT: ENGELMANN, Hartmut
: TITLE OF INVENTION: TNF INHIBITORS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/800,909
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/476,862
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 94039
: FILING DATE: 06-APR-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 91229
: FILING DATE: 06-AUG-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 90339
: FILING DATE: 18-MAY-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.

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;
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-09-800-909-1

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 2
US-09-800-908-2/C
; Sequence 2, Application US/09800908
; Patent No. US2002011462A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; BIGDA, Jacek
; BELETSKY, Igor
; METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,908
; FILING DATE: 08-Mar-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,347
; FILING DATE: <unknown>
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-800-908-2

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 3
US-09-954-456-1187/C
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1187
; LENGTH: 3683
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1187

Query Match 100.0%; Score 20; DB 10; Length 3683;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 4
US-09-764-869-1332
; Sequence 1332, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
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; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1332
; LENGTH: 23432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1332

Query Match 84.0%; Score 16.8; DB 10; Length 23432;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
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DB 10830 TCACAGAGAGCAGGGACTT 10849

RESULT 5

US-09-962-436-281/c
; Sequence 281, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 281
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-281

Query Match 82.0%; Score 16.4; DB 10; Length 167343;
Best Local Similarity 94.4%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACAGAGAGTCAGGGACTT 20
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DB 23246 ACAGAGAGCAGGGACTT 23229

RESULT 6

US-09-964-824A-273/c
; Sequence 273, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horriagan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-964-824A-273

Query Match 82.0%; Score 16.4; DB 10; Length 167343;
Best Local Similarity 94.4%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACAGAGAGTCAGGGACTT 20
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DB 23246 ACAGAGAGCAGGGACTT 23229

RESULT 7

US-09-981-876-66
; Sequence 66, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
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; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,582
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,596
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,612
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,632
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,601
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/043,580
 ; PRIOR FILING DATE: 1997-04-11
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 ; PRIOR FILING DATE: 1997-04-11
 ; PRIOR APPLICATION NUMBER: 60/048,974
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/056,886
 ; PRIOR FILING DATE: 1997-08-22
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 ; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/056,864
 ; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/056,631
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 ; PRIOR FILING DATE: 05-Sep-1997
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 ; PRIOR FILING DATE: 1997-04-11
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 ; PRIOR FILING DATE: 1997-08-22
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 ; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/048,964
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/057,650
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/056,884
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 66
 ; LENGTH: 3301

Query Match 79.0%; Score 15.8; DB 9; Length 3301;
 Best Local Similarity 89.5%; Pred. No. 92;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCACAGAGATCAGGACT 19

Db 432 TCAGAGAGAGTCAGGGAGT 450
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RESULT 8

US-09-764-847-1719
; Sequence 1719, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1719
; LENGTH: 6019
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1719

Query Match 79.0%; Score 15.8; DB 10; Length 6019;
Best Local Similarity 89.5%; Pred. No. 99;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACAGAGAGTCAGGGAGT 20
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Db 207 CACAGGGAGTCAGGGAGT 225

RESULT 9

US-09-764-860-895/c
; Sequence 895, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 895
; LENGTH: 9581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-895

Query Match 79.0%; Score 15.8; DB 10; Length 9581;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACAGAGAGTCAGGGAGT 20
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Db 6204 CACAGAGGTCAGGGAGT 6186

RESULT 10

US-09-764-846-306
; Sequence 306, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 306
; LENGTH: 32204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-846-306

Query Match 77.0%; Score 15.4; DB 10; Length 32204;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACAGAGAGTCAGGGAC 18
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Db 3996 CACAGAGACTCAGGGAC 4012

RESULT 11

US-09-864-761-30451/c
; Sequence 30451, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30451
; LENGTH: 155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL078471.2

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79
; OTHER INFORMATION: NT HIT: AL163201.2, EVALUE 2.00e-82
; OTHER INFORMATION: EST_HUMAN HIT: AAB37753.1, EVALUE 8.00e-24
; OTHER INFORMATION: SWISSPROT HIT: O77681, EVALUE 6.60e+00
US-09-864-761-30451

Query Match 76.0%; Score 15.2; DB 10; Length 155;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGACTT 20
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Db 84 TCAAAGAGAGTCAGGCGCTT 65

RESULT 12

US-09-938-842A-2494
; Sequence 2494, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2494
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2494

Query Match 76.0%; Score 15.2; DB 9; Length 285;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGATCAGGACTT 20
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Db 140 TCACAGAGCGTCGGGACTT 159

RESULT 13

US-09-867-701-302/c
; Sequence 302, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FASTSEQ for Windows version 4.0
; SEQ ID NO 302
; LENGTH: 333
; TYPE: DNA

; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(333)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-302

Query Match 76.0%; Score 15.2; DB 10; Length 333;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGATCAGGACTT 20
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Db 173 TCACAGAGGTCAGGACTT 154

RESULT 14

US-09-853-386-31
; Sequence 31, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; FILE REFERENCE: P01972US1
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 406
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(406)
; OTHER INFORMATION: n equals unknown
US-09-853-386-31

Query Match 76.0%; Score 15.2; DB 10; Length 406;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGATCAGGACTT 20
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Db 367 TCACAGAGACACAGGCGCTT 386

RESULT 15

US-09-864-761-13882/c
; Sequence 13882, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03


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; PRIOR APPLICATION NUMBER: CB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13882
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL078471.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79
US-09-864-761-13882

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Query Match          76.0%; Score 15.2; DB 10; Length 474;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
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Db 365 TCAAAGAGACTGAGGCGCTT 346

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Search completed: December 6, 2002, 00:19:59
Job time : 118.972 secs

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QY 757 TTTGTTGTTGTTGTTGTTTCCCTCCCTGGCTCTG-CCAGCTCTGGCTTCCAGAAACC 815
Db 1830 TTTGTTGTTGTTGTTGTTTCTCCCTGGCTCTGCCCCAGCTCTGGCTTCCAGAAACC 1889
QY 816 CCAGCATCTTTTCTGCAGAGGGCTTCTGCAGAGGGATCGCTGAGTCACCCA 875
Db 1890 CCAGCATCTTTTCTGCAGAGGGCTTCTGCAGAGGGATCGCTGAGTCACCCA 1949
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Db 1950 TGAAGACAGGACGTGCTTACAGCTGAGCTGAGCTGCGGATGCTGGGCTCTGT 2009
QY 936 GTAGGAGGAGGTGGAGCCCTGTAGGAAAGCGGGTCTCTCAAGTTAGCTCAGGAGCTT 995
Db 2010 GTAGGAGGAGGTGGAGCCCTGTAGGAAAGCGGGTCTCTCAAGTTAGCTCAGGAGCTT 2069
QY 996 GGAAGCATCATCCTCAGGCGAGGTGCTGCTCAGCTATGATCCAGACCTTTGGGA 1055
Db 2070 GGAAGCATCATCCTCAGGCGAGGTGCTCAGCTATGATCCAGACCTTTGGGA 2129
QY 1056 GGCTGAGCGGGTGGATCAGCTGAGGTAGGATTCGAGACCGCTTGGCCAAACATGGTA 1115
Db 2130 GGCTGAGCGGGTGGATCAGCTGAGGTAGGATTCGAGACCGCTTGGCCAAACATGGTA 2189
QY 1116 AAACCCATCTCTACTATAAATAACAGAAATAGCCGGGCTGGTGGGCGACCTATAGT 1175
Db 2190 AAACCCATCTCTACTATAAATAACAGAAATAGCCGGGCTGGTGGGCGACCTATAGT 2249
QY 1176 CCAGCTACTCAGAGCCTGAGCTGGGAAATCGTTTGAACCGGGAAGCGGAGTTGCA 1235
Db 2250 CCAGCTACTCAGAGCCTGAGCTGGGAAATCGTTTGAACCGGGAAGCGGAGTTGCA 2309
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Db 2310 GGGAGCGGAGATCAGGCACTGCACCTCCAGCCTGGGCGACAGAGAGTGTCTCAA 2369
QY 1296 AAGAAAAA 1310
Db 2370 AAGAAAAA 2384

RESULT 11
AAQ10907
ID AAQ10907 standard; cDNA; 2393 BP.
XX
AC AAQ10907;
XX
XX
DT 13-MAY-1991 (first entry)
XX
DE 40kD TNF inhibitor precursor gene in c40dk#6.
XX
KW Tumour necrosis factor; inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 93..1478
FT /*tag= a
XX
XX
PN AU058976-A.
XX
PD 24-JAN-1991.
XX
PF 16-JUL-1990; 90AU-0058976.
XX
PR 07-FEB-1990; 90US-0479661.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.

(SYNE-) SYNERGEN INC.
WPI: 1991-073847/11.
P-PSDB; AAR11001.
Tumour necrosis factor inhibitor - for suppression of TNF-alpha
and -beta, useful as therapeutic agent.
Disclosure; Fig 39; 142pp; English.
The sequence encodes the entire 40 kD TNF inhibitor. The clone from
CC which the sequence was obtd. was isolated from a cDNA library
CC prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
CC gene can be inserted into expression vectors for prep'n. of TNF
CC inhibitor for use in the treatment of inflammatory and degenerative
CC diseases.
CC See also AAQ10878, AAQ10884 and AAQ10883.
XX Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;
SQ
Query Match 44.4%; Score 1159; DB 12; Length 2393;
Best Local Similarity 98.2%; Pred. No. 1.1e-299;
Matches 1193; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
QY 97 GACCCCCACCCCATCTTGTCTTAGCAGATTCTTCCCTGGTGGCCATGGGACCCAGGTC 156
Db 1170 GAGGCGCGGGCAGCACCGGAGCTCAGATTCTTCCCTGGTGGCCATGGGACCCAGGTC 1229
QY 157 AATGTCACCTCGCATCGTAACGCTCTGTAGCAGCTCTGACACAGCTCACAGTGTCTCTCC 216
Db 1230 AATGTCACCTCGCATCGTAACGCTCTGTAGCAGCTCTGACACAGCTCACAGTGTCTCTCC 1289
QY 217 CAAGCCAGCTCCACAATGGGAGACACAGATTCCAGCCCTCGGAGTCCCGAAGGAGCAG 276
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Db 1350 CAGGTCCCTTCTCCAGAGGAGGAATGCTTTCGGTACAGCTGGAGAGCCGAGAGACC 1409
QY 337 CTGCTGGGAGCACGAAAGAGAGCCCTTCCCTTGGAGTGGCTGAGCCCTTGGCAGG 396
Db 1410 CTGCTGGGAGCACGAAAGAGAGCCCTTCCCTTGGAGTGGCTGAGCCCTTGGCAGG 1469
QY 397 CCCAGTTAACCCAGGCGGCTGTGGCTGTGCTAGCAGCAAGGTGGCTGAGCCCTTGGCAGG 456
Db 1470 CCCAGTTAACCCAGGCGGCTGTGGCTGTGCTAGCAGCAAGGTGGCTGAGCCCTTGGCAGG 1529
QY 457 ATGACCTTGGGAGGCGCTGTGCTTCCAGGCGCCACCACTAGGACTCTGAGGCTCT 516
Db 1530 ATGACCTTGGGAGGCGCTGTGCTTCCAGGCGCCACCACTAGGACTCTGAGGCTCT 1588
QY 517 TTCTGGGCCAAGTCTCTAGTCCCTTCCAGCCGAGCCTCCCTCTGACCTGAGGCGC 576
Db 1589 TTCTGGGCCAAGTCTCTAGTCCCTTCCAGCCGAGCCTCCCTCTGACCTGAGGCGC 1648
QY 577 AAGAGCAGGCGAGCGAGTGGGGAAGGCTCTGCTGCCATGCTGCTCTCCGGAAG 636
Db 1649 AAGAGCAGGCGAGCGAGTGGGGAAGGCTCTGCTGCCATGCTGCTCTCCGGAAG 1708
QY 637 GCTGGCTGGGCATGGAGCTTGGGGGATGCTGGGGCAAGTCCCTGACTCTCTGAGCTCT 696
Db 1709 GCTGGCTGGGCATGGAGCTTGGGGGATGCTGGGGCAAGTCCCTGACTCTCTGAGCTCT 1768
QY 697 CCCCAGCCAGCTGCACCTGCGAGCCTGCTTGGAGCCCTTGGGTTTGTGTTGTTG 756
Db 1769 CCCCAGCCAGCTGCACCTGCGAGCCTGCTTGGAGCCCTTGGGTTTGTGTTGTTGTTG 1828
QY 757 TTTGTTTGTGTTGTTGTTTCTCCCTGGGCTCTG-CCAGCTCTGGCTTCCAGAAACC 815
Db 1829 TTTGTTTGTGTTGTTGTTTCTCCCTGGGCTCTGCCCGAGCTCTGGCTTCCAGAAACC 1888

tumour necrosis factor (TNF) receptor ligand - used to increase

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 628.284 Seconds
(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937A-1
Perfect score: 2613
Sequence: 1 tctgtctcgtctcctgcg.....cctgtttgttttaaaaaa 2613

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2613	100.0	2613	21 AAA49207	Human tumour necro
2	2493	95.4	3683	24 ABK83997	Human cDNA differe
3	2493	95.4	3683	24 ABK65877	Lung cancer relate
4	2493	95.4	3683	24 ABK33465	Human TNF receptor
5	2493	95.4	3683	24 ABK33466	Human TNF receptor
6	2493	95.4	3683	24 ABK33467	Human TNF receptor
7	1423	54.5	2339	12 AAQ10956	Encodes human 75kD
8	1423	54.5	2339	20 AAZ09171	Human tumour necro
9	1423	54.5	2339	22 AAH48860	Human TNFBP-associ

10	1171	44.8	2394	22 AAC83951	Human 40 kDa TNF 1
11	1159	44.4	2393	12 AAQ10907	40kD TNF inhibitor
12	1022.8	39.1	2224	16 AAQ89544	p75 Tumour Necrosi
c 13	613.2	23.5	733	24 ABK83541	Human cDNA differe
14	453	17.3	1641	14 AAQ49931	TNF-R cDNA. Homo
15	453	17.3	1641	15 AAQ45224	Sequence encoding
16	441	16.9	1640	12 AAQ10990	Partial sequence o
c 17	337.8	12.9	455	22 AAH83437	Human ovarian tumo
c 18	336	12.9	336	22 AAS24803	Human ovarian PCR-
c 19	245.2	9.4	618	22 AAQ62220	Human immune/haema
c 20	244.8	9.4	119950	20 AAX90201	Human immune/haema
c 21	244	9.3	27154	22 AAL05708	Human ves1 gene.
c 22	243.2	9.3	2932	13 AAQ25388	Human reproductive
c 23	243.2	9.3	2932	20 AAZ32161	Human thromboxane
c 24	243.2	9.3	2932	20 AAZ32162	Human endothelial
c 25	243.2	9.3	2932	23 AAS65879	DNA encoding novel
c 26	243.2	9.3	2932	24 ABK83654	Human cDNA differe
c 27	242.6	9.3	2500	22 ABK94360	Human full-length
c 28	242	9.3	589	22 AAK73475	Human immune/haema
c 29	241.8	9.3	14848	22 ABAL5454	Human nervous syst
c 30	241.8	9.3	17542	22 ABAL5453	Human nervous syst
c 31	241.2	9.2	122888	24 ABK83569	Human cDNA differe
c 32	241	9.2	3234	16 AAQ92781	Human thymopoietin
c 33	241	9.2	4125	22 AAK84260	Human immune/haema
c 34	241	9.2	4129	22 AAK84261	Human immune/haema
c 35	240.8	9.2	22609	22 AAL35781	Human musculoskele
c 36	240.8	9.2	32193	22 ABQ88849	Human prostate exp
c 37	240.2	9.2	827	24 ABQ88849	cDNA encoding colo
38	240	9.2	240	24 ABK45619	Human immune/haema
39	240	9.2	26390	22 AAK65971	Human nervous syst
c 40	240	9.2	27869	22 ABAL19635	Human immune/haema
c 41	240	9.2	27869	22 AAK66517	Human immune/haema
c 42	239.8	9.2	825	22 AAK86384	Human cDNA differe
c 43	239.8	9.2	43599	24 ABK84242	Human protein comp
c 44	239.6	9.2	1296	19 AAV29031	Human immune/haema
45	239.6	9.2	12500	22 AAK77971	Human immune/haema

ALIGNMENTS

RESULT 1
AAA49207
ID AAA49207 standard; DNA; 2613 BP.
XX
AC AAA49207;
XX
DT 22-NOV-2000 (first entry)
DE Human tumour necrosis factor alpha receptor 2 gene exon 10.
DE Human tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW osteoporosis; ds.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT
FT Location/Qualifiers
FT 1..2613
FT /*tag= a
FT /product= "TNFR2"
FT /partial
FT replace (593,A), (598,G), (620,T)
FT /*tag= b
FT /label= allele_1
FT replace (593,A), (598,T), (620,T)
FT /*tag= c
FT /label= allele_2
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FT /*tag= d
FT /label= allele_3
FT replace (593,G), (598,T), (620,T)
FT /*tag= e
FT /label= allele_4

```
XX PA (HYSE-) HYSEQ INC.
XX PI
XX DR Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB: ABG23902.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1: SEQ ID NO 23893; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 448 BP; 86 A; 141 C; 130 G; 91 T; 0 other;

Query Match 80.9%; Score 17.8; DB 23; Length 448;
Best Local Similarity 90.5%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACTCA 21
    ||||| ||||| ||||| |||||
Db 167 GTGAAGTCAAGATGACCTCA 147

RESULT 9
ID AAS88094/c
XX AAS88094 standard; cDNA; 474 BP.
XX AC AAS88094;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #23898.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
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```
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB: ABG23907.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1: SEQ ID NO 23898; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 474 BP; 88 A; 158 C; 130 G; 98 T; 0 other;

Query Match 80.9%; Score 17.8; DB 23; Length 474;
Best Local Similarity 90.5%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACTCA 21
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Db 266 GTGAAGTCAAGATGACCTCA 246

RESULT 10
ID AAD22561
XX AAD22561 standard; DNA; 651 BP.
XX AC AAD22561;
XX DT 29-JAN-2002 (first entry)
XX DE Human FDRG (fibrinogen domain related) related DNA.
XX KW Human; FDRG; fibrinogen domain related protein; signal transduction;
XX KW homeostasis; thermogenesis; adiposity; lipolysis; lipogenesis; obesity;
XX KW vasculogenesis; angiogenesis; wound healing; cardiovascular disorder;
XX KW hyperinsulinaemia; diabetes; atherosclerosis; cancer; tumour; cachexia;
XX KW gene therapy; anorectic; vulnery; immunomodulator; cytostatic;
XX KW appetite; glucose metabolism; ds.
XX OS Homo sapiens.
XX FH Key
XX FT CDS Location/Qualifiers
XX FT 1..651
XX FT /*tag= a
XX FT /product= "Human FDRG (fibrinogen domain related)
XX FT related protein"
XX FT /note= "CDS does not include both start and stop
XX FT codon"
XX FT /partial
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XX PN WO200177151-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-US11400.
XX PR 07-APR-2000; 2000US-0546547.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA (DAND) DANA FARBER CANCER INST INC.
XX PI Holtzman DA, Spiegelman BM, Yoon CH;
XX DR WPI: 2002-010893/01.
XX DR P-PSDB; AAE13522.
XX PT Novel fibrinogen domain related polypeptides and polynucleotides useful
XX PT as modulating agents in regulating angiogenesis, metabolism-related
XX PT processes and for treating hematopoietic and proliferative disorders -
XX PT Disclosure; Page 147; 169pp; English.
XX PS The invention relates to novel FDRG (fibrinogen domain related) proteins
XX CC and their corresponding nucleic acids. FDRG or its modulator is useful
XX CC for activation of FDRG-dependent signal transduction pathway, modulation
XX CC of angiogenesis, haematopoiesis, development or differentiation of a
XX CC FDRG-expressing cell (e.g. mediation of growth and/or differentiation
XX CC of adipocytes, white adipocytes or brown adipocytes), proliferation,
XX CC development or differentiation of non-FDRG-expressing cell, insulin
XX CC of a (non) FDRG-expressing cell, insulin sensitivity and/or insulin
XX CC responsiveness, insulin secretion, cell recruitment, glucose metabolism,
XX CC maintenance of energy homeostasis (e.g. regulating the balance and/or
XX CC imbalance between energy storage and energy expenditure, for e.g.
XX CC increasing/decreasing energy expenditure), regulation of adaptive
XX CC thermogenesis (e.g. regulation of the biogenesis of mitochondria,
XX CC expression of mitochondrial enzymes, expression of uncoupling proteins),
XX CC regulation of adiposity, lipolysis, lipogenesis, modulation of the
XX CC efficiency of energy storage, regulation of appetite, vasculogenesis,
XX CC tumour angiogenesis, wound healing and expansion/reduction of tumour and
XX CC fat mass. FDRG or its modulator is useful for regulating, preventing
XX CC and/or treating obesity, diseases or disorders that accompany obesity
XX CC (e.g. cardiovascular disorders), metabolic abnormalities typical of
XX CC obesity (hyperinsulinaemia), diabetes, disorders of energy homeostasis,
XX CC insulin resistance, disorders associated with lipid metabolism (e.g.
XX CC cachexia), atherosclerosis, disorders associated with abnormal
XX CC vasculogenesis (e.g. cancers, including cancers of the epithelia e.g.
XX CC carcinomas of the pancreas, stomach, liver, secretory glands, bladder,
XX CC lung, breast, skin), reproductive tract and cancers of the
XX CC haematopoietic, immune system and nervous system. FDRG DNA is used in
XX CC gene therapy. The present sequence is human FDRG related DNA.
XX SQ Sequence 651 BP; 129 A; 203 C; 203 G; 116 T; 0 other;
Query Match 80.9%; Score 17.8; DB 24; Length 651;
Best Local Similarity 90.5%; Pred. No. 83;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GTGATCTCGAGACTCA 21
||||| ||||||||| |||||
Db 91 GTGAAGTCAAGACTCA 111
RESULT 11
AAD22560
ID AAD22560 standard; cDNA; 1143 BP.
XX AC AAD22560;
XX AC AAD22560;
XX DT 29-JAN-2002 (first entry)
XX DE Human mature FDRG (fibrinogen domain related) protein encoding cDNA.
XX XX

KW Human; FDRG; fibrinogen domain related protein; signal transduction;
KW homeostasis; thermogenesis; adiposity; lipolysis; lipogenesis; obesity;
KW vasculogenesis; angiogenesis; wound healing; cardiovascular disorder;
KW hyperinsulinaemia; diabetes; atherosclerosis; cancer; tumour; cachexia;
KW gene therapy; anorectic; vulnery; immunomodulator; cytostatic;
XX appetite; glucose metabolism; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 1..1143
XX FT /*tag= a
XX FT /product= "Human mature FDRG (fibrinogen domain
XX FT related) protein"
XX PN WO200177151-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-US11400.
XX PR 07-APR-2000; 2000US-0546547.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA (DAND) DANA FARBER CANCER INST INC.
XX PI Holtzman DA, Spiegelman BM, Yoon CH;
XX DR WPI: 2002-010893/01.
XX DR P-PSDB; AAE13521.
XX PT Novel fibrinogen domain related polypeptides and polynucleotides useful
XX PT as modulating agents in regulating angiogenesis, metabolism-related
XX PT processes and for treating hematopoietic and proliferative disorders -
XX PS Claim 2; Fig 2; 169pp; English.
XX CC The invention relates to novel FDRG (fibrinogen domain related) proteins
XX CC and their corresponding nucleic acids. FDRG or its modulator is useful
XX CC for activation of FDRG-dependent signal transduction pathway, modulation
XX CC of angiogenesis, haematopoiesis, development or differentiation of a
XX CC FDRG-expressing cell (e.g. mediation of growth and/or differentiation
XX CC of adipocytes, white adipocytes or brown adipocytes), proliferation,
XX CC development or differentiation of non-FDRG-expressing cell, insulin
XX CC of a (non) FDRG-expressing cell, insulin sensitivity and/or insulin
XX CC responsiveness, insulin secretion, cell recruitment, glucose metabolism,
XX CC maintenance of energy homeostasis (e.g. regulating the balance and/or
XX CC imbalance between energy storage and energy expenditure, for e.g.
XX CC increasing/decreasing energy expenditure), regulation of adaptive
XX CC thermogenesis (e.g. regulation of the biogenesis of mitochondria,
XX CC expression of mitochondrial enzymes, expression of uncoupling proteins),
XX CC regulation of adiposity, lipolysis, lipogenesis, modulation of the
XX CC efficiency of energy storage, regulation of appetite, vasculogenesis,
XX CC tumour angiogenesis, wound healing and expansion/reduction of tumour and
XX CC fat mass. FDRG or its modulator is useful for regulating, preventing
XX CC and/or treating obesity, diseases or disorders that accompany obesity
XX CC (e.g. cardiovascular disorders), metabolic abnormalities typical of
XX CC obesity (hyperinsulinaemia), diabetes, disorders of energy homeostasis,
XX CC insulin resistance, disorders associated with lipid metabolism (e.g.
XX CC cachexia), atherosclerosis, disorders associated with abnormal
XX CC vasculogenesis (e.g. cancers, including cancers of the epithelia e.g.
XX CC carcinomas of the pancreas, stomach, liver, secretory glands, bladder,
XX CC lung, breast, skin), reproductive tract and cancers of the
XX CC haematopoietic, immune system and nervous system. FDRG DNA is used in
XX CC gene therapy. The present sequence is a cDNA encoding human mature
XX CC FDRG protein.
XX SQ Sequence 1143 BP; 232 A; 373 C; 356 G; 182 T; 0 other;
Query Match 80.9%; Score 17.8; DB 24; Length 1143;
Best Local Similarity 90.5%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
 DB 565 GTGAACTGCAAGATGAACCTCA 585

RESULT 12
 AAD22559

ID AAD22559 standard; cDNA; 1218 BP.
 XX
 AC AAD22559;
 XX
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human FDRG (fibrinogen domain related) protein encoding cDNA fragment.
 XX
 KW Human; FDRG; fibrinogen domain related protein; signal transduction;
 KW homeostasis; thermogenesis; adiposity; lipolysis; lipogenesis; obesity;
 KW vasculogenesis; angiogenesis; wound healing; cardiovascular disorder;
 KW hyperinsulinaemia; diabetes; atherosclerosis; cancer; tumour; cachexia;
 KW gene therapy; anorectic; vulnary; immunomodulator; cytostatic;
 KW appetite; glucose metabolism; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200177151-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-US11400.
 XX
 XX 07-APR-2000; 2000US-0546547.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Holtzman DA, Spiegelman BM, Yoon CH;
 XX
 DR WP1; 2002-010893/01.
 XX
 XX Novel fibrinogen domain related polypeptides and polynucleotides useful
 PT as modulating agents in regulating angiogenesis, metabolism-related
 PT processes and for treating hematopoietic and proliferative disorders -
 XX
 XX Claim 2; Page 142-143; 169pp; English.
 XX
 CC The invention relates to novel FDRG (fibrinogen domain related) proteins
 CC and their corresponding nucleic acids. FDRG or its modulator is useful
 CC for activation of FDRG-dependent signal transduction pathway, modulation
 CC of angiogenesis, haematopoiesis, development or differentiation of a
 CC FDRG-expressing cell (e.g. mediation of growth and/or differentiation
 CC of adipocytes, white adipocytes or brown adipocytes), proliferation,
 CC development or differentiation of non-FDRG-expressing cell, homeostasis
 CC of a (non) FDRG-expressing cell, insulin sensitivity and/or insulin
 CC responsiveness, insulin secretion, cell recruitment, glucose metabolism,
 CC maintenance of energy homeostasis (e.g. regulating the balance and/or
 CC imbalance between energy storage and energy expenditure, for e.g.
 CC increasing/decreasing energy expenditure), regulation of adaptive
 CC thermogenesis (e.g. regulation of the biogenesis of mitochondria,
 CC expression of mitochondrial enzymes, expression of uncoupling proteins),
 CC regulation of adiposity, lipolysis, lipogenesis, modulation of the
 CC efficiency of energy storage, regulation of appetite, vasculogenesis,
 CC tumour angiogenesis, wound healing and expansion/reduction of tumour and
 CC fat mass. FDRG or its modulator is useful for regulating, preventing
 CC and/or treating obesity, diseases or disorders that accompany obesity
 CC (e.g. cardiovascular disorders), metabolic abnormalities typical of
 CC obesity (hyperinsulinaemia), diabetes, disorders of energy homeostasis,
 CC insulin resistance, disorders associated with lipid metabolism (e.g.
 CC cachexia), atherosclerosis, disorders associated with abnormal
 CC vasculogenesis (e.g. cancers, including cancers of the epithelia e.g.
 CC carcinomas of the pancreas, stomach, liver, secretory glands, bladder,
 CC lung, breast, skin), reproductive tract and cancers of the
 CC haematopoietic, immune system and nervous system. FDRG DNA is used in
 CC gene therapy. The present sequence is human FDRG cDNA fragment.

XX
 SQ Sequence 1218 BP; 241 A; 401 C; 383 G; 193 T; 0 other;
 Query Match 80.9%; Score 17.8; DB 24; Length 1218;
 Best Local Similarity 90.5%; Pred. NO. 92;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;
 QY 1 GTGATCTGCAAGATGAACCTCA 21
 DB 640 GTGAACTGCAAGATGAACCTCA 660

RESULT 13
 AA297139

ID AA297139 standard; DNA; 1221 BP.
 XX
 AC AA297139;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE Human gene 75 DNA sequence, SEQ ID NO:448.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; gene 75; chromosome 19; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO9966041-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 15-JUN-1999; 99WO-US13418.
 XX
 PR 16-JUN-1998; 98US-0089507.
 PR 16-JUN-1998; 98US-0089508.
 PR 16-JUN-1998; 98US-0089509.
 PR 16-JUN-1998; 98US-0089510.
 PR 22-JUN-1998; 98US-0090112.
 PR 22-JUN-1998; 98US-0090113.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
 PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsu G;
 XX
 DR WPI; 2000-106100/09.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Disclosure; Page 159; 586pp; English.
 XX
 CC AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 CC AA297019 to AA297137 are the secreted proteins encoded by the 94 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC e.g., by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 94 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin

CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
 CC disorders, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The sequences shown in AAY86334 to AAY86585 represent fragments of the
 CC secreted proteins, and the sequences shown in AAZ97138 and AAZ97139
 CC represent gene 75 nucleotide sequences.

XX
 SQ Sequence 1221 BP; 242 A; 400 C; 385 G; 194 T; 0 other;

Query Match 80.9%; Score 17.8; DB 21; Length 1221;
 Best Local Similarity 90.5%; Pred. NO. 92;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGAACCTCA 21
 |||| ||||||||| |||||
 Db 640 GTGAAGTGCAGATGACCTCA 660

RESULT 14
 AAZ97132
 ID AAZ97132 standard; cDNA; 1379 BP.
 XX
 AC AAZ97132;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE Human secreted protein gene 75 cDNA clone HDRM182, SEQ ID NO:124.
 XX
 KW Human: secreted protein; cancer; tumour; developmental abnormality;
 KW foetal disease; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO9966041-A1.
 PN
 XX 23-DEC-1999.
 PD
 XX 15-JUN-1999; 99WO-US13418.
 PF
 XX 16-JUN-1998; 98US-0089507.
 PR 16-JUN-1998; 98US-0089508.
 PR 16-JUN-1998; 98US-0089509.
 PR 16-JUN-1998; 98US-0089510.
 PR 22-JUN-1998; 98US-0090112.
 PR 22-JUN-1998; 98US-0090113.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Ni J., Rosen CA, Wei Y, Young PE, Florence KA;
 PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsuouli G;
 XX
 XX WPI: 2000-106100/09.
 DR P-PSDB: AAY86328.
 XX
 XX New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 XX Claim 1: Page 384; 586pp; English.

CC AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes.
 CC AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC e.g., by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample

CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 94 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
 CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
 CC disorders, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The sequences shown in AAY86334 to AAY86585 represent fragments of the
 CC secreted proteins.

XX
 SQ Sequence 1379 BP; 313 A; 398 C; 431 G; 237 T; 0 other;

Query Match 80.9%; Score 17.8; DB 21; Length 1379;
 Best Local Similarity 90.5%; Pred. NO. 94;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGAACCTCA 21
 |||| ||||||||| |||||
 Db 273 GTGAAGTGCAGATGACCTCA 293

RESULT 15
 ABQ88100
 ID ABQ88100 standard; cDNA; 1413 BP.
 XX
 AC ABQ88100;
 XX
 DT 18-SEP-2002 (first entry)
 XX
 DE Human osteoblast differentiation related cDNA SEQ ID NO 7.
 DE Human: osteoblast; stem cell differentiation; bone tissue deposition;
 XX osteoporosis; osteopathic; ss.
 KW
 KW Homo sapiens.
 OS
 XX WO200250301-A2.
 PN
 XX 27-JUN-2002.
 PD
 XX 18-DEC-2001; 2001WO-US48276.
 PF
 XX 18-DEC-2000; 2000US-255882P.
 PR 24-APR-2001; 2001US-285891P.
 PR
 XX (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 XX
 XX Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
 PI Mertz L;
 PI
 XX WPI: 2002-557663/59.
 DR
 XX Use of genes and their expression profiles associated with osteoblast
 PT differentiation for screening modulators bone formation, for diagnosing
 PT or treating e.g. osteoporosis, or as markers for the differentiation
 PT process -
 XX
 XX Claim 1: SEQ ID NO 7; 78pp + Sequence Listing; English.
 PS
 XX The invention relates to genes and their expression profiles are used
 CC for:
 CC (a) screening modulators of precursor stem cell differentiation into
 CC osteoblasts, or bone tissue deposition;
 CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
 CC osteoblast formation or osteoporosis; or
 CC (c) treating or monitoring treatment of the conditions cited in (b), or
 CC monitoring the progression of bone tissue deposition.
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,

CC drug-induced abnormalities in bone formation or bone loss, conditions
 CC that involve altered bone metabolism (e.g. idiopathic juvenile
 CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
 CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
 CC osteoblast differentiation associated cDNA marker of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 xx

SQ Sequence 1413 BP; 278 A; 463 C; 444 G; 228 T; 0 other;

Query Match 80.9%; Score 17.8; DB 24; Length 1413;
 Best Local Similarity 90.5%; Pred. No. 94;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
 |||||
 Db 704 GTGACTGCAAGATGACCTCA 724

Search completed: December 5, 2002, 23:29:56
 Job time : 39.2898 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 : Search time 42.1061 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937a-2

Perfect score: 22

Sequence: 1 gtgatctgcaagatgaactcac 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	DB ID	Description
1	18.8	85.5	482	17	AQ817730	AQ817730 HS-5250_B
2	17.8	80.9	78	13	BJ062060	BJ062060 BJ062060
3	17.8	80.9	240	9	AV249962	AV249962 AV249962
4	17.8	80.9	305	14	M62290	M62290 EST00364 Hi
5	17.8	80.9	353	14	T08223	T08223 EST06114 In
6	17.8	80.9	400	12	BF023606	BF023606 5 Human H

7	17.8	80.9	424	14	T33835	T33835 EST59446 Hu
8	17.8	80.9	484	9	AA122061	AA122061 zk93b12. r
c 9	17.8	80.9	493	10	BE215937	BE215937 HV_CEB000
10	17.8	80.9	509	14	BM967237	BM967237 I132c02 y
c 11	17.8	80.9	521	17	BH360315	BH360315 CH230-107
12	17.8	80.9	527	14	BM967022	BM967022 Ij29d10.y
c 13	17.8	80.9	561	13	BM179919	BM179919 dai13d02.
c 14	17.8	80.9	576	9	AJ498267	AJ498267 AJ498267
c 15	17.8	80.9	586	17	BH351116	BH351116 CH230-198
c 16	17.8	80.9	608	13	BJ107879	BJ107879 BJ107879
c 17	17.8	80.9	610	9	A1556475	A1556475 UI-R-C2p-
c 18	17.8	80.9	627	12	BF005034	BF005034 EST433532
c 19	17.8	80.9	631	10	AW956861	AW956861 EST368931
c 20	17.8	80.9	644	17	BH033878	BH033878 RPCI-24-3
c 21	17.8	80.9	680	9	AL648363	AL648363 AL648363
c 22	17.8	80.9	702	12	BG583307	BG583307 EST485058
c 23	17.8	80.9	812	17	AZ703920	AZ703920 RPCI-23-2
24	17.8	80.9	841	14	BO881023	BO881023 AGENCOURT
25	17.8	80.9	859	17	CNS03GKF	AL243096 Tetraodon
26	17.8	80.9	893	13	BI192811	BI192811 602945042
c 27	17.4	79.1	163	9	AA192559	AA192559 zq02e04. s
c 28	17.4	79.1	228	17	AQ580761	AQ580761 RPCI-11-4
c 29	17.4	79.1	321	10	AW382482	AW382482 CM1-HT033
c 30	17.4	79.1	336	12	BE708615	BE708615 MR0-HT055
c 31	17.4	79.1	344	14	Z29781	Z29781 ATTS2225 Or
c 32	17.4	79.1	349	10	AW509663	AW509663 ga62a12.y
33	17.4	79.1	364	12	BF989328	BF989328 IL5-GN017
c 34	17.4	79.1	393	14	BQ359828	BQ359828 CM0-HN020
c 35	17.4	79.1	398	10	BE168428	BE168428 OV3-HT051
c 36	17.4	79.1	467	10	AW699768	AW699768 g031h02.y
c 37	17.4	79.1	509	13	BJ180510	BJ180510 BJ180510
c 38	17.4	79.1	512	13	BJ159235	BJ159235 BJ159235
39	17.4	79.1	518	13	BJ172933	BJ172933 BJ172933
40	17.4	79.1	520	9	AL120881	AL120881 DKFZp762M
41	17.4	79.1	539	10	AW382320	AW382320 CM1-HT032
42	17.4	79.1	561	10	AV830290	AV830290 AV830290
43	17.4	79.1	561	13	BJ172163	BJ172163 BJ172163
c 44	17.4	79.1	569	13	BJ187317	BJ187317 BJ187317
c 45	17.4	79.1	574	13	BJ193124	BJ193124 BJ193124

ALIGNMENTS

RESULT 1	AQ817730	AQ817730	482 bp	DNA	linear	GSS 26-AUG-1999
LOCUS	HS_5250_B1_C07_SP6E	RPCI-11 Human Male	BAC Library	Homo sapiens		
DEFINITION	genomic clone	Plate-826 Col-13	Row=F	DNA sequence.		
ACCESSION	AQ817730					
VERSION	AQ817730.1	GI:5780123				
KEYWORDS	GSS.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	1 (bases 1 to 482)					
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,					
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and					
	Hood,L.					
TITLE	Sequence-tagged connectors: A sequence approach to mapping and					
	scanning the human genome					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	96 (17)	9739-9744	(1999)		
MEDLINE	99380589					
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L					
	High Throughput Sequencing Center					
	University of Washington					
	401 Queen Anne Avenue North, Seattle, WA 98109, USA					
	Tel: (206) 616-3618					
	Fax: (206) 616-3887					
	Email: jwallace@u.washington.edu					
	Clones are derived from the human BAC library RPCI-11. For BAC					
	library availability, please contact Pieter de Jong					

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 826 row: F column: 13
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 482.
 Location/Qualifiers
 1. .482

FEATURES

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-826 Col-13 Row-F"

/clone_lib="RPC1-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

98 a 137 c 107 g 131 t 9 others

BASE COUNT

ORIGIN

Query Match 85.5%; Score 18.8; DB 17; Length 482;

Best Local Similarity 90.9%; Pred. No. 3.le+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCAC 22

|||||

Db 308 GTGGTCTGCAAGATGAACCTCAC 329

RESULT 2

BJ062060

LOCUS

DEFINITION BJ062060 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL074006 5', mRNA sequence. EST 11-DEC-2001

ACCESSION BJ062060

VERSION BJ062060.1 GI:17499724

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 78)

Kitayama.A., Terasaka.C., Mochii.M., Ueno.N., Shin-I.T. and Kohara

Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasu Shin-I

Center for Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

FEATURES

source

Location/Qualifiers

1. .78

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="XL074006"

/clone_lib="NIBB Mochii normalized Xenopus tailbud library"

/tissue_type="whole embryo"

/dev_stage="stage 25"

/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs

were oligo-dT primed and directionally cloned. Staging

according to Nieuwkoop and Faber. Library is subtracted

and was constructed by N. Garrett and A.M. Zorn,

(Wellcome/CRC Institute)."

BASE COUNT

ORIGIN

23 a 17 c 16 g 20 t 2 others

Query Match 80.9%; Score 17.8; DB 13; Length 78;
 Best Local Similarity 90.5%; Pred. No. 4.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGATCTGCAAGATGAACCTCAC 22

|||||

Db 38 TGCTCTGGAAGATGAACCTCAC 58

RESULT 3

AV249962/c

LOCUS

DEFINITION AV249962 RIKEN full-length enriched, 0 day neonate head Mus musculus cDNA clone 483420C07 3', similar to X84797 M. musculus mRNA similar to human hematopoietic specific protein 1, mRNA sequence. EST 04-NOV-1999

ACCESSION AV249962

VERSION AV249962.1 GI:6237421

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 240)

Konno.H., Aizawa.K., Akahira.S., Akiyama.J., Carninci.P., Endo.T.,

Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N., Hirozane.T., Hori.F.,

Ishii.Y., Ishikawa.T., Itoh.M., Izawa.M., Kadota.K., Kagawa.I., Kai

.C., Kawai.J., Kikuchi.N., Kojima.Y., Koya.S., Kusakabe.M.,

Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y.,

Owa.C., Ozawa.Y., Saito.H., Sano.M., Sato.K., Shibata.K., Shibata

.Y., Shigenoto.Y., Shiraki.T., Sogabe.Y., Sugahara.Y., Suzuki.H.,

Suzuki.H., Takahashi.F., Tateo.M., Tominaga.N., Tsunoda.Y.,

Watanabe.S., Yamamura.T., Yasunishi.A., Yokota.T.,

Yoshiki.A., Yoshino.M., Muramatsu.M. and Hayashizaki.Y.

RIKEN Mouse ESTs (Konno.H., et al. 1999)

Unpublished (1999)

Contact: Yoshihide Hayashizaki

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Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>,

Sasaki.N., Izawa.M., Watanabe.M., Okazaki.Y. and Hayashizaki

.Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh.M., Kitsunai.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J.,

Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu.M., Okazaki

.Y. and Hayashizaki.Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci.P. and Hayashizaki.Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

Location/Qualifiers

1. .240

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="483420C07"

/clone_lib="RIKEN full-length enriched, 0 day neonate

head"

/sex="mixed"

/tissue_type="head"

/dev_stage="0 day neonate"

/lab_host="DH10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Columbia University, P & S
630 W168th St., New York, NY 10032, USA
Tel: 212 305 3441
Fax: 212 305 4262
Email: pbfl@columbia.edu
Insert Length: 400 Std Error: 0.00
POLYA=No.

FEATURES
Source Location/Qualifiers
1. .400
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="mda-D-47"
/cell_lib="Human HO-1 melanoma cells"
/cell_type="HO-1 melanoma cells"
/note="Vector: pPripLEX2; Site_1: sf1A; Site_2: sf1B"

BASE COUNT 94 a 116 c 122 g 68 t
ORIGIN

Query Match 80.9% Score 17.8; DB 12; Length 400;
Best local similarity 90.5% Pred. No. 8.2e+02;
Matches 19: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGACTCTGCAGATGAACCTCA 21
||||| ||||||| ||||| |||||
Db 292 GTGAACCTGCAAGATGACCTCA 312

RESULT 7
T33835

LOCUS T33835 424 bp mRNA linear EST 06-SEP-1995
DEFINITION EST59446 Human Brain Homo sapiens cDNA 5' end similar to None, mRNA sequence.

ACCESSION T33835
VERSION T33835.1 GI:615933
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 424)
Adams,M.D., Kerlavage,A.R., Fleischmann,K.G., Gocayne,J.D., Bult
C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., White
O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A.,
Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,P.S., Kelley,J.M.,
Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,
Dinke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W.,
Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L.,
Kunsch,C., Ji,H., Li,H., Messinger,P.S., Olsen,H., Raymond,L., Wei
Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THC9268
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers

```

Query Match      80.9%; Score 17.8; DB 9; Length 484;
Best Local Similarity 90.5%; Pred. No. 8.8e-02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CTGATCTGCAAGATGAACCTCA 21
    |||| ||||| ||||| |||||
Db 44 CTGAACCTGCAAGATGACCTCA 64

RESULT 9
BE215937/c
LOCUS      BE215937              493 bp      mRNA      linear      EST 23-OCT-2001
DEFINITION HV_CEB0008007f Hordeum vulgare seedling green leaf EST library
            HV_CEB0008007f (Blumeria challenged) Hordeum vulgare cDNA clone
ACCESSION   BE215937
VERSION     BE215937.2 GI:13264649
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
ORGANISM    Hordeum vulgare.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
            ; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 493)
AUTHORS    Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
            Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Chol
            ,D.W., Fenton,R.D., Oates,R. and Main,D.
            Development of a genetically and physically anchored EST resource
            for barley genomics: Blumeria infected incompatible (Mla6) seedling
            leaf cDNA library
            Unpublished (2001)
            On Jul 3, 2000 this sequence version replaced gi:8903549.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 447
            High quality sequence stop: 488.
FEATURES             source
     1..493
         /organism="Hordeum vulgare"
         /cultivar="C116151 (Mla6)"
         /db_xref="taxon:4513"
         /clone="HV_CEB0008007f"
         /clone_lib="Hordeum vulgare seedling green leaf EST
         /library HVcDNA0005 (Blumeria challenged)"
         /tissue_type="seedling green leaf"
         /lab_host="SOLR"
         /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
         C.I. 16151 (Mla6) plants were greenhouse grown in the R
         Wise lab at Iowa State University, Ames, IA; 7 day old
         green seedlings were challenged with isolate 5874 (AvrMla6
         ) of Blumeria graminis f. sp. hordei, and leaves were
         harvested 20 and 24 hr post-inoculation and snap frozen;
         uninoculated leaves were harvested 20 hr post-inoculation
         (Wei, Wise). In the TJ Close lab at the University of
         California, Riverside, total RNA was prepared from each
         sample pool, equal quantities of all three RNA pools were
         combined, poly(A) RNA was purified from the mixture, one
         pfu were in vivo excised to give pBluescript SK(-) cDNA
         phagemids (Choi, Close). Phagemids were plated and picked
         at the Clemson University Genomics Institute (CUGI) (Begum
         , Palmer, Frisch, Atkins and Wing). Plasmid DNA
         preparations, DNA sequencing and sequence analysis were
         performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
         , Rambo, Main). The sequence has been trimmed to remove
         vector sequence and contains a minimum of 100 bases of

```

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phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders/Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*

BASE COUNT      115 a 148 c 143 g 86 t 1 others
ORIGIN

Query Match      80.9%; Score 17.8; DB 10; Length 493;
Best Local Similarity 90.5%; Pred. No. 8.9e-02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGATCTGCAAGATGAACCTCA 21
    ||||| ||||| ||||| |||||
Db 427 GTGATCTCCAAGAGGAACCTCA 407

RESULT 10
BM967237
LOCUS      BM967237              509 bp      mRNA      linear      EST 29-APR-2002
DEFINITION ij32c02.yl Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
            CDNA clone IMAGE:6136322 5' similar to TR:Q9Y5B3 Q9Y5B3
            ANGIOPOIETIN-RELATED PROTEIN. ;, mRNA sequence.
ACCESSION   BM967237
VERSION     BM967237.1 GI:19561026
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 509)
            Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blinston,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
            Jackson,Y. and Bowers,Y.
            Endocrine Pancreas Consortium
            Unpublished (2000)
            Other_ESTs: ij32c02.xl
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohph.harvard.edu
            Library was constructed by Dr. Douglas Melton DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Juliana Brown
            (brown@fas.harvard.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     1..509
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:6136322"
         /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
         /sex="Both"
         /tissue_type="Islets of Langerhans"
         /dev_stage="Adult"
         /lab_host="DH10B"
         /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
         Site_2: Sal 1; Starting library constructed using
         SuperScript Plasmid Library kit (Life Technologies). cDNA
         made by oligo-dt priming. Size-selected by column
         fractionation; average insert size 1.08 kb. Library was
         amplified once on solid support and plasmid DNA from

```

library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 99 a 161 c 161 g 88 t

Query Match 80.9%; Score 17.8; DB 14; Length 509;
Best Local Similarity 90.5%; Pred. No. 9e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGATCTGCAAGATGAACCTCA 21

Db 23 GTGACTGCAAGATGAACCTCA 43

RESULT 11
BH360315/C

LOCUS 521 bp DNA linear GSS 03-DEC-2001
DEFINITION CH230-107F8.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-107F8, DNA sequence.

ACCESSION BH360315

VERSION BH360315.1 GI:17291049

KEYWORDS GSS.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

1 (bases 1 to 521)

Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,

A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de

Jong, P., and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Unpublished (1999)

Other_GSSs: CH230-107F8.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Plate: 107 row: F column: 8

Seq primer: T7

Class: BAC ends.

FEATURES Location/Qualifiers

1..521

/organism="Rattus norvegicus"

/strain="BN/SsNHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-107F8"

/clone_lib="CHORI-230 Segment 1"

/sex="Female"

/cell_type="Brain"

/note="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;

CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by

Pieter de Jong"

BASE COUNT 80 a 106 c 127 g 208 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 17; Length 521;

Best Local Similarity 90.5%; Pred. No. 9e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGATCTGCAAGATGAACCTCA 21

Db 462 GTGACTGCAAGATGAACCTCA 442

RESULT 12
BM967022

LOCUS 527 bp mRNA linear EST 29-APR-2002

DEFINITION ij29d10.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

CDNA clone IMAGE:6136003 5' similar to TR:Q9Y5B3 Q9Y5B3

ANGIOTENSIN-RELATED PROTEIN. ; mRNA sequence.

ACCESSION BM967022

VERSION BM967022.1 GI:19560624

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 527)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas

, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.

, Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other_ESTs: ij29d10.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Juliana Brown

(brown@fas.harvard.edu)

Seq primer: -40Rp from Gibco

High quality sequence stop: 451.

FEATURES Location/Qualifiers

1..527

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6136003"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;

Site_2: Sal 1; Starting library constructed using

SuperScript Plasmid Library kit (Life Technologies). cDNA

made by oligo-dr priming. Size-selected by column

fractionation; average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from

library was prepared. The library DNA was normalized by

method #4 from Bonaldo, Lennon, and Soares 1996 Genome

Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product

representing library inserts and hybridized to an EcoT of

20. Single-stranded (unhybridized) plasmids were isolated

by hydroxyapatite chromatography and used to make this

library."

BASE COUNT 105 a 163 c 166 g 93 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 14; Length 527;

Best Local Similarity 90.5%; Pred. No. 9.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
 Db 23 GTGAATGCAAGATGAACCTCA 43
 IIII IIII IIII IIII IIII

RESULT 13
 LOCUS BM179919
 DEFINITION dail3d02.yl NICHD XGC Emb4 Xenopus laevis cDNA clone IMAGE:4959386
 mRNA sequence.
 ACCESSION BM179919
 VERSION BM179919.1 GI:17403990
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 561)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 447.
 Location/Qualifiers
 1..561
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:4959386"
 /clone_lib="NICHD XGC Emb4"
 /dev_stage="embryo, stage 31-32"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site_1:
 NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
 dT. Average insert size 2.1 kb. Constructed by Life
 Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."
 BASE COUNT 145 a 128 c 121 g 167 t
 ORIGIN

Query Match 80.9%; Score 17.8; DB 13; Length 561;
 Best Local Similarity 90.5%; Pred. No. 9.3e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCATCTGCAAGATGAACCTCAC 22
 Db 498 TCCTCTGGAAGATGAACCTCAC 518
 II IIII IIII IIII IIII IIII

RESULT 14
 LOCUS AJ498267/c
 DEFINITION AJ498267 MTP0SE Medicago truncatula cDNA clone mt--acc955202h09,
 mRNA sequence.
 ACCESSION AJ498267
 VERSION AJ498267.1 GI:22088710
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eusoids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 576)
 Firnhaber, C., Bartelsmeier, V., Meyer, F., Bartels, D., Bekel, T.,
 Linke, B., Puehler, A. and Kuester, H.
 Determination of transcript sequences from developing pods
 including seeds of Medicago truncatula genotype Al7
 Unpublished (2002)
 Contact: Kuester H
 Lehrstuhl fuer Genetik
 Universitaet Bielefeld
 Postfach 100131, D-33501 Bielefeld, Germany.
 Location/Qualifiers
 1..576
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="mt--acc955202h09"
 /clone_lib="MTP0SE"
 /tissue_type="pods including seeds"
 /dev_stage="different stages of development"
 /note="Vector: pGEM-T; Site_1: PstI; Site_2: SphI;
 genotype Al7; cDNA was prepared from polyA+ enriched RNA
 from developing pods including seeds harvested at
 different stages of development. The cDNA was
 directionally ligated by Medigenomix into the pGEM-T
 vector from Promega using GCATGCCGCCGAGCGCCGACATG and
 CTCAGGCCATTATGCCGG adapters. Plasmids containing cDNA
 inserts were propagated in E. coli DH10B cells."
 BASE COUNT 139 a 114 c 133 g 190 t
 ORIGIN

Query Match 80.9%; Score 17.8; DB 9; Length 576;
 Best Local Similarity 90.5%; Pred. No. 9.4e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATCTGCAAGATGAACCTCAC 22
 Db 315 TGAGCTGCAAGATGAACACAC 295
 III IIII IIII IIII IIII IIII

RESULT 15
 LOCUS BH351116/c
 DEFINITION BH351116 586 bp DNA linear GSS 03-DEC-2001
 CH230-198M8 TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
 CH230-198M8, DNA sequence.
 BH351116
 ACCESSION BH351116
 VERSION BH351116.1 GI:17281850
 KEYWORDS GSS.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 586)
 Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
 A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
 Jong, P. and Fraser, C.M.
 Rat BAC End Sequences from Library CHORI-230 EcoRI segment
 Unpublished (1999)
 Other_GSSs: CH230-198M8.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pletier de Jong (pdejong@email.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or_ering_information.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html


```

Plate: 198 row: M column: 8
Seq primer: SP6
Class: BAC ends.
FEATURES
    source
        1. .586
            /organism="Rattus norvegicus"
            /strain="BN/SSNHsd/MCH"
            /db_xref="taxon:10116"
            /clone="CH230-198M8"
            /clone_lib="CHORI-230 Segment 1"
            /sex="Female"
            /cell_type="Brain"
            /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
            CHORI-230 Rat (BN/SSNHsd/MCH) BAC library produced by
            Pieter de Jong"
BASE COUNT      92 a   134 c   147 g   213 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 17; Length 586;
Best Local Similarity 90.5%; Pred. No. 9.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Uy 1 GTGATCTGCAAGATGAATCA 21
    ||||| ||||| ||||| |||||
Db 447 GTGACCTGCATGATGAATCA 427

Search completed: December 6, 2002, 04:54:09
Job time : 56.1061 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 : Search time 1.14286 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-2

Perfect score: 22

Sequence: 1 gtgatctgcaagatgaactcac 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17.8	80.9	1869	3	US-08-934-494-1
2	17.8	80.9	1869	3	US-09-143-068-1
3	17.8	80.9	1869	4	US-09-143-707-1
4	17.8	80.9	1869	4	US-09-202-089-1
5	17.8	80.9	1869	4	US-09-511-133-1
6	17.8	80.9	1869	4	US-09-690-169-1
7	17.8	80.9	1869	4	US-09-511-631-1
8	16.4	74.5	4440	3	US-07-792-600-1
9	16.4	74.5	4440	3	US-09-157-021-1
10	16.4	74.5	4440	3	US-09-156-842-1
11	16.4	74.5	5433	3	US-09-157-021-35
12	16.4	74.5	5433	3	US-09-156-842-35
13	16.2	73.6	571	4	US-09-404-879A-102
14	16.2	73.6	2045	1	US-08-379-926A-7
15	16.2	73.6	8533	1	US-07-846-181-6
16	16.2	73.6	8533	1	US-07-845-989-6
17	16.2	73.6	9763	3	US-08-973-273-1
18	15.8	71.8	499	1	US-07-935-311A-1
19	15.8	71.8	499	1	US-08-368-079-1
20	15.8	71.8	499	5	PCT-US93-07996-1
21	15.8	71.8	2840	5	PCT-US93-06251-64
22	15.8	71.8	4868	1	US-08-139-937-12
23	15.8	71.8	4868	5	PCT-US93-11310-12
24	15.8	71.8	8789	1	US-08-328-254-5
25	15.8	71.8	10136	1	US-08-353-700-2
26	15.8	71.8	10136	5	PCT-US95-16216-2
27	15.6	70.9	1272	2	US-08-972-258-1

c 28	15.6	70.9	1272	4	US-09-263-128-1	Sequence 1, Appli
c 29	15.6	70.9	1523	2	US-08-713-636-1	Sequence 1, Appli
c 30	15.6	70.9	2346	4	US-09-193-503B-4	Sequence 4, Appli
c 31	15.6	70.9	2346	4	US-09-193-503B-5	Sequence 5, Appli
c 32	15.6	70.9	2346	4	US-09-193-503B-8	Sequence 8, Appli
c 33	15.4	70.0	54	4	US-08-679-645-634	Sequence 634, App
c 34	15.4	70.0	55	1	US-07-869-380B-2	Sequence 2, Appli
c 35	15.4	70.0	64	1	US-07-869-380B-1	Sequence 1, Appli
c 36	15.2	69.1	685	3	US-08-881-094-14	Sequence 14, Appli
c 37	15.2	69.1	1991	4	US-08-235-836C-69	Sequence 69, Appli
c 38	15.2	69.1	1991	4	US-08-235-836C-77	Sequence 77, Appli
c 39	15.2	69.1	2665	4	US-08-971-089-5	Sequence 5, Appli
c 40	15.2	69.1	5211	1	US-08-447-411-1	Sequence 1, Appli
c 41	15.2	69.1	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c 42	14.8	67.3	255	4	US-08-952-736B-3	Sequence 3, Appli
c 43	14.8	67.3	718	4	US-08-998-416-638	Sequence 638, App
c 44	14.8	67.3	948	4	US-09-134-001C-949	Sequence 949, App
c 45	14.8	67.3	996	1	US-07-757-390-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-934-494-1
; Sequence 1, Application US/08934494
; Patent No. 6030831
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,494
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1869 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-934-494-1

Query Match 80.9%; Score 17.8; DB 3; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21

||||| ||||| ||||| |||||

Db 803 GTGAAGTCAAGATGACCTCA 823

RESULT 2

US-09-143-068-1

```

: Sequence 1, Application US/09143068
: Patent No. 6074873
: GENERAL INFORMATION:
: APPLICANT: Fong, Sherman
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth
: APPLICANT: Williams, Mickey
: TITLE OF INVENTION: Tie Ligand Homologues
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/143,068
: FILING DATE: 28-Aug-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Dreger, Ginger R.
: REGISTRATION NUMBER: 33,055
: REFERENCE/DOCKET NUMBER: P1078P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-3216
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1869 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: US-09-143-068-1

Query Match 80.9%; Score 17.8; D
Best local similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches

QY 1 GTGATCTGCAAGATGAACTCA 21
|||||
DB 803 GTGACTGCAAGATGAACTCA 823

RESULT 3
US-09-143-707-1
: Sequence 1, Application US/09143707
: Patent No. 6346350
: GENERAL INFORMATION:
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Tie Ligands
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,707
; FILING DATE: 28-Aug-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1078R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1869 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-09-143-707-1

Query Match      80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
    ||||| ||||| ||||| |||||
Db 803 GTGAACCTGCAAGATGACCTCA 823

RESULT 4
US-09-202-089-1
; Sequence 1, Application US/09202089
; Patent No. 6348351
; GENERAL INFORMATION:
; APPLICANT: Genentech Inc.
; APPLICANT: Fong, Sherman
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth
; APPLICANT: Williams, Mickey
; TITLE OF INVENTION: Tie Ligand Homologues
; FILE REFERENCE: P1078P2(e)
; CURRENT APPLICATION NUMBER: US/09/202,089
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: PCT/US98/19094
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 08/934,494
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-202-089-1

Query Match      80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
    ||||| ||||| ||||| |||||
Db 803 GTGAACCTGCAAGATGACCTCA 823

RESULT 5
US-09-511-133-1
; Sequence 1, Application US/095111133
; Patent No. 6372491
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; FILE REFERENCE: P1078R1C1
; CURRENT APPLICATION NUMBER: US/09/511.133
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 09/143,707
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 60/059,352
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-511-133-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
||||| ||||||| |||||
Db 803 GTGAAGTCAAGATGACCTCA 823

RESULT 6

US-09-690-169-1
; Sequence 1, Application US/09690169
; Patent No. 6426218
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: TIE LIGANDS
; FILE REFERENCE: GENENT 58A2D2
; CURRENT APPLICATION NUMBER: US/09/690,169
; CURRENT FILING DATE: 2001-09-04
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 09/143,707
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/059,352
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-690-169-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
||||| ||||||| |||||
Db 803 GTGAAGTCAAGATGACCTCA 823

RESULT 7

US-09-511-631-1
; Sequence 1, Application US/09511631
; Patent No. 6455496
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; FILE REFERENCE: P1078R1D1
; CURRENT APPLICATION NUMBER: US/09/511.631
; CURRENT FILING DATE: 2000-02-23
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 09/143,707
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 60/059,352

; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-511-631-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
||||| ||||||| |||||
Db 803 GTGAAGTCAAGATGACCTCA 823

RESULT 8

US-07-792-600-1/c
; Sequence 1, Application US/07792600
; Patent No. 6008045
; GENERAL INFORMATION:
; APPLICANT: COPELAND, WILLIAM C.
; APPLICANT: WANG, TERESA S.-F.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMAIC SYNTHESIS OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Peter G. Carroll
; STREET: 220 Montgomery Street, Suite 710
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/792,600
; FILING DATE: 19911115
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: STDU-00097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4440 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-792-600-1

Query Match 74.5%; Score 16.4; DB 3; Length 4440;
Best Local Similarity 94.4%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGATCTGCAAGATGAACCT 19
||||| ||||||| |||||
Db 2282 TGATCTGCAAGATGAACCT 2265

RESULT 9

US-09-157-021-1/c
; Sequence 1, Application US/09157021A
; Patent No. 6100023
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.

```
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Design Assay
; FILE REFERENCE: STDU-03484
; CURRENT APPLICATION NUMBER: US/09/157,021A
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 07/792,600
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-157-021-1

Query Match      74.5%; Score 16.4; DB 3; Length 4440;
Best Local Similarity 94.4%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 10
US-09-156-842-1/c
; Sequence 1, Application US/09156842A
; Patent No. 6103473
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Screening
; FILE REFERENCE: STDU-03485
; CURRENT APPLICATION NUMBER: US/09/156,842A
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 07/792,600
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-156-842-1

Query Match      74.5%; Score 16.4; DB 3; Length 4440;
Best Local Similarity 94.4%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 11
US-09-157-021-35/c
; Sequence 35, Application US/09157021A
; Patent No. 6100023
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Design Assay
; FILE REFERENCE: STDU-03484
; CURRENT APPLICATION NUMBER: US/09/157,021A
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 07/792,600
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5433
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-156-842-35/c
; Sequence 35, Application US/09156842A
; Patent No. 6103473
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Screening
; FILE REFERENCE: STDU-03485
; CURRENT APPLICATION NUMBER: US/09/156,842A
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 07/792,600
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-156-842-35

Query Match      74.5%; Score 16.4; DB 3; Length 5433;
Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 12
US-09-156-842-35/c
; Sequence 35, Application US/09156842A
; Patent No. 6103473
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Screening
; FILE REFERENCE: STDU-03485
; CURRENT APPLICATION NUMBER: US/09/156,842A
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 07/792,600
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-156-842-35

Query Match      74.5%; Score 16.4; DB 3; Length 5433;
Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 13
US-09-404-879A-102
; Sequence 102, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-102

Query Match      73.6%; Score 16.2; DB 4; Length 571;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GTGATCTGCAAGATGAAC 21
Db  356 GTGACCTGGAAGAAGAACTCA 376

RESULT 14
US-08-379-926A-7/c
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; Sequence 7, Application US/08379926A
; Patent No. 5783414
; GENERAL INFORMATION:
; APPLICANT: CARREZ, DIRK
; APPLICANT: ROOS, JOEL
; TITLE OF INVENTION: EXPRESSION SYSTEM, INTEGRATION
; TITLE OF INVENTION: VECTOR
; TITLE OF INVENTION: VECTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,926A
; FILING DATE: 27-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09400102
; FILING DATE: 28-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09400586
; FILING DATE: 17-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09500014
; FILING DATE: 09-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 3987-13-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2045 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-379-926A-7

Query Match 73.6%; Score 16.2; DB 1; Length 2045;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAAGTCA 21
Db 1377 GTATTCGAGGATGAAGTCA 1357

RESULT 15
US-07-846-181-6/c
; Sequence 6, Application US/07846181
; Patent No. 5360732
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REV, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/846,181
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC204-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-846-181-6

Query Match 73.6%; Score 16.2; DB 1; Length 8533;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAAGTCA 21
Db 1298 GTATTCGAGGATGAAGTCA 1278

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Job time : 8.14286 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run On: December 5, 2002, 20:03:23 ; Search time 1.06939 Seconds
(without alignments)
8021.899 Million cell updates/sec

Title: US-09-856-937A-2

Perfect score: 22

Sequence: 1 gtgactctgaagatgaactcac 22

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Searched: 350425 seqs, 194966369 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	17.4	79.1	543	10	US-09-924-401-33
4	17.4	79.1	3103	10	US-09-925-302-85
5	17.4	79.1	5185	9	US-09-870-759-94
6	17.7	77.3	1850	10	US-09-822-830A-576
7	17.7	77.3	2570	12	US-10-036-342-17
8	17.7	77.3	2570	12	US-10-006-867-167
9	16.8	76.4	1503841	9	US-09-946-807-1
10	16.8	76.4	1503841	10	US-09-795-668-1
11	16.8	76.4	1503841	10	US-09-795-668-1
12	16.4	74.5	481	10	US-09-864-761-5696
13	16.2	73.6	302	10	US-09-560-863-683
14	16.2	73.6	571	10	US-09-884-441-102
15	15.8	71.8	470	10	US-09-864-761-1050
16	15.8	71.8	1004	9	US-09-938-842A-3644
17	15.8	71.8	1358	10	US-09-789-561-47
18	15.8	71.8	1493	9	US-09-992-598-134
19	15.8	71.8	1493	9	US-09-989-293A-134

C 20	15.8	71.8	1493	10	US-09-989-722-134	Sequence 134, App
C 21	15.8	71.8	1493	10	US-09-989-723-134	Sequence 134, App
C 22	15.8	71.8	1493	10	US-09-989-727-134	Sequence 134, App
C 23	15.8	71.8	1493	10	US-09-989-729-134	Sequence 134, App
C 24	15.8	71.8	1493	10	US-09-989-731-134	Sequence 134, App
C 25	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 26	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 27	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 28	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 29	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 30	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 31	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 32	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 33	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 34	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 35	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 36	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 37	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 38	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 39	15.6	70.9	5233	10	US-09-815-242-6760	Sequence 154, App
C 40	15.6	70.9	5233	10	US-09-815-242-6760	Sequence 154, App
C 41	15.6	70.9	5233	10	US-09-815-242-6760	Sequence 154, App
C 42	15.6	70.9	5233	10	US-09-815-242-6760	Sequence 154, App
C 43	15.6	70.9	5233	10	US-09-815-242-6760	Sequence 154, App
C 44	15.4	70.0	933	9	US-10-027-806-43	Sequence 43, Appl
C 45	15.4	70.0	32998	9	US-10-027-806-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-10-000-512-5
; Sequence 5, Application US/10000512
; Patent No. US20020164699A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A
; APPLICANT: Fernandes, Elma
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAME
; FILE REFERENCE: 15966-556
; CURRENT APPLICATION NUMBER: US/10/000,512
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/619,252
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/167,785
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(1368)
US-10-000-512-5

Query Match 80.9% Score 17.8; DB 9; Length 1855;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
Db 790 GTGAAGTCAAGATGACCTCA 810

RESULT 2
US-09-919-172-49
; Sequence 49, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.

;
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
;
; FILE REFERENCE: PA-0036 US
;
; CURRENT APPLICATION NUMBER: US/09/919,172
;
; PRIOR FILING DATE: 2001-07-30
;
; PRIOR APPLICATION NUMBER: 60/222,469
;
; PRIOR FILING DATE: 2000-07-28
;
; NUMBER OF SEQ ID NOS: 102
;
; SOFTWARE: PERL Program
;
; SEQ ID NO 49
;
; LENGTH: 3936
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: misc.feature
;
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1088524.8
;
; NAME/KEY: unsure
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; LOCATION: 2060-2170, 3796, 3799, 3816
;
; OTHER INFORMATION: a, t, c, g, or other
;
US-09-919-172-49

Query Match 80.9%; Score 17.8; DB 10; Length 3936;
Best Local Similarity 90.5%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACTCA 21
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DB 871 GTGAAGTCAAGATCACTCA 891

RESULT 3

US-09-924-401-33/C
; Sequence 33, Application US/09924401
; Patent No. US20020142957A1
; GENERAL INFORMATION:
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.550
; CURRENT APPLICATION NUMBER: US/09/924,401
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 38, 451, 509, 537
; OTHER INFORMATION: n = A,T,C or G
;
US-09-924-401-33

Query Match 79.1%; Score 17.4; DB 10; Length 543;
Best Local Similarity 94.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACT 19
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DB 215 GTGATTTGCAAGATCACT 197

RESULT 4

US-09-925-302-85
; Sequence 85, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302

;
; CURRENT FILING DATE: 2001-08-10
;
; PRIOR APPLICATION NUMBER: PCT/US00/05918
;
; PRIOR FILING DATE: 2000-03-08
;
; PRIOR APPLICATION NUMBER: 60/124,270
;
; PRIOR FILING DATE: 1999-03-12
;
; NUMBER OF SEQ ID NOS: 896
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 85
;
; LENGTH: 3103
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: misc.feature
;
; LOCATION: (293)
;
; OTHER INFORMATION: n equals a,t,g, or c
;
US-09-925-302-85

Query Match 79.1%; Score 17.4; DB 10; Length 3103;
Best Local Similarity 94.7%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACT 19
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DB 904 GTGATTTGCAAGATCACT 922

RESULT 5

US-09-870-759-94
; Sequence 94, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 5185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(4474)
; OTHER INFORMATION:
;
US-09-870-759-94

Query Match 79.1%; Score 17.4; DB 9; Length 5185;
Best Local Similarity 94.7%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATCTGCAAGATCACTCAC 22
||||| ||||||| |||||
DB 1556 ATCTGCAAGATCAATCAC 1574

RESULT 6

US-09-822-830A-576
; Sequence 576, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 576
; LENGTH: 1850

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 2;

; OTHER INFORMATION: n=a,c,g, or t

US-09-822-830A-576

Query Match 77.3%; Score 17; DB 10; Length 1850;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GATCTCGAAGTGAAGT 19

|||||

DB 617 GATCTCGAAGTGAAGT 633

RESULT 7

US-10-036-342-17

; Sequence 17, Application US/10036342

; Patent No. US20020090681A1

; GENERAL INFORMATION:

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Watanabe, Collin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3030R1C5

; CURRENT APPLICATION NUMBER: US/10/036,342

; CURRENT FILING DATE: 2001-12-26

; PRIOR APPLICATION NUMBER: 60/085579

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/112514

; PRIOR FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: 60/113300

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: 60/113430

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/113605

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/114140

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/115552

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/116843

; PRIOR FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: 60/125774

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/125778

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/125826

; PRIOR FILING DATE: 1999-03-24

; PRIOR APPLICATION NUMBER: 60/127035

; PRIOR FILING DATE: 1999-03-31

; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800

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: PRIOR FILING DATE: 2001-06-01
: PRIOR APPLICATION NUMBER: PCT/US01/16692
: PRIOR FILING DATE: 2001-06-20
: PRIOR APPLICATION NUMBER: PCT/US01/21066
: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: PCT/US01/21735
: PRIOR FILING DATE: 2001-07-09
: NUMBER OF SEQ ID NOS: 80
: SEQ ID NO 17
: LENGTH: 2570
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-036-342-17

Query Match      77.3%; Score 17; DB 12; Length 2570;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GATCTGCAAGTGAAC 19
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Db      1294 GATCTGCAAGTGAAC 1310

RESULT 8
US-10-006-867-167
: Sequence 167, Application US/10006867
: Patent No. US20020119130A1
: GENERAL INFORMATION:
: APPLICANT: Eaton, Dan L.
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3230R1C1
: CURRENT APPLICATION NUMBER: US/10/006,867
: CURRENT FILING DATE: 2001-12-06
: PRIOR APPLICATION NUMBER: 60/063435
: PRIOR FILING DATE: 1997-10-29
: PRIOR APPLICATION NUMBER: 60/064215
: PRIOR FILING DATE: 1997-10-29
: PRIOR APPLICATION NUMBER: 60/082797
: PRIOR FILING DATE: 1998-04-22
: PRIOR APPLICATION NUMBER: 60/083495
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/085579
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/087759
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/088021
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088029
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088030
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088734
: PRIOR FILING DATE: 1998-06-10
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: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088811
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088824
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: PRIOR APPLICATION NUMBER: 60/088825
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088863
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/089105
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/089514
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089653
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089952
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/090246
: PRIOR FILING DATE: 1998-06-22
: PRIOR APPLICATION NUMBER: 60/090444
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090688
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: PRIOR APPLICATION NUMBER: 60/090696
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090862
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/091628
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/096012
: PRIOR FILING DATE: 1998-08-10
: PRIOR APPLICATION NUMBER: 60/096757
: PRIOR FILING DATE: 1998-08-17
: PRIOR APPLICATION NUMBER: 60/096949
: PRIOR FILING DATE: 1998-08-18
: PRIOR APPLICATION NUMBER: 60/096959
: PRIOR FILING DATE: 1998-08-18
: PRIOR APPLICATION NUMBER: 60/097954
: PRIOR FILING DATE: 1998-08-26
: PRIOR APPLICATION NUMBER: 60/097971
: PRIOR FILING DATE: 1998-08-26
: PRIOR APPLICATION NUMBER: 60/097979
: PRIOR FILING DATE: 1998-08-26
: PRIOR APPLICATION NUMBER: 60/098749
: PRIOR FILING DATE: 1998-09-01
: PRIOR APPLICATION NUMBER: 60/099741
: PRIOR FILING DATE: 1998-09-10
: PRIOR APPLICATION NUMBER: 60/099763
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: PRIOR APPLICATION NUMBER: 60/099792
: PRIOR FILING DATE: 1998-09-10
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: PRIOR FILING DATE: 1998-09-10
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: PRIOR FILING DATE: 1998-09-10
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: PRIOR APPLICATION NUMBER: 60/100930
: PRIOR FILING DATE: 1998-09-17
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: PRIOR FILING DATE: 1998-09-22
: PRIOR APPLICATION NUMBER: 60/101475
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: PRIOR APPLICATION NUMBER: 60/101738
: PRIOR FILING DATE: 1998-09-24
: PRIOR APPLICATION NUMBER: 60/101743
: PRIOR FILING DATE: 1998-09-24
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: PRIOR FILING DATE: 1998-09-24
: PRIOR APPLICATION NUMBER: 60/102570
: PRIOR FILING DATE: 1998-09-30
: PRIOR APPLICATION NUMBER: 60/103449
: PRIOR FILING DATE: 1998-10-06
: PRIOR APPLICATION NUMBER: 60/103678
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: PRIOR APPLICATION NUMBER: 60/103679
: PRIOR FILING DATE: 1998-10-08
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; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
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; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106030
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106856
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/106807
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112419
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112422
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; PRIOR APPLICATION NUMBER: 60/112853
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113011
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/112854
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113408
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114223
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/115614
; PRIOR FILING DATE: 1999-01-12
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; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119525
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
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; PRIOR APPLICATION NUMBER: 60/129674
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/173481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142

Query Match          77.3%; Score 17; DB 12; Length 2570;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      3 GATCTGCAAGATGAAC 19
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Db      1294 GATCTGCAAGATGAAC 1310
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RESULT 9
US-09-946-807-1/c
; Sequence 1, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946.807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795.668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515.716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r-g or a
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y-t/u or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m-a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k-g or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w-a or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b-g or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d-a or g or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
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; OTHER INFORMATION: h=a or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1

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Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATCTGCAAGATGAACCTCA 21
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Db 1305659 TGATGTGCAAGATTAACCTCA 1305640

RESULT 10

US-09-795-668-1/c
; Sequence 1, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)

; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1

Query Match 76.4%; Score 16.8; DB 10; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATCTGCAAGATGAACCTCA 21
||||| ||||||| |||||||
Db 1305659 TGATGTGCAAGATTAACCTCA 1305640

RESULT 11

US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1

Query Match 76.4%; Score 16.8; DB 10; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATCTGCAAGATGAACCTCA 21

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Best Local Similarity 94.4%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGATCTGCAAGATGAACCT 19
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Db 79 TGATCTGCAATATGAACCT 62

RESULT 13
US-09-560-863-683
; Sequence 683, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020110809A1 Human Polynucleotides and the
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: LEX-0018-USA
; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 302
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(302)
; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-683

Query Match 73.6%; Score 16.2; DB 10; Length 302;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
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Db 144 GTGCTGCAAGTTGAACCTTA 164

RESULT 14
US-09-884-441-102
; Sequence 102, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-884-441-102

Query Match 73.6%; Score 16.2; DB 10; Length 571;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
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Db 356 GTGACCTGGAAGAACTCA 376

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RESULT 15
US-09-864-761-1050/c
; Sequence 1050, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1050
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008159.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; NAME/KEY: unsure
; LOCATION: 57
; NAME/KEY: unsure
; LOCATION: 256
US-09-864-761-1050

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Best Local Similarity 89.5%; Pred. No. 1.le+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 465 GTGACCTGCAAGATGAATT 447
Search completed: December 6, 2002, 00:17:39
Job time : 1463.07 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: December 5, 2002, 23:30:25 ; Search time 41.4471 Seconds
(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937A-3
Perfect score: 20
Sequence: 1 acaccagctctgatgtttca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
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- 35: em_htg_rod:*
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- 37: em_htg_vrt:*
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- 39: em_btg_hum:*
- 40: em_btg_mus:*
- 41: em_btg_other:*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	20	100.0	106	9	HSTNFR2S05	U52160 Human tumor
C 2	20	100.0	199	9	AB030950	AB030950 Homo sapi
C 3	20	100.0	691	6	I36350	I36350 Sequence 12
C 4	20	100.0	705	6	ARI17443	ARI17443 Sequence
C 5	20	100.0	1080	9	HUMTNFRA	M35857 Human tumor
C 6	20	100.0	1557	6	AX054825	AX054825 Sequence
C 7	20	100.0	1557	6	I36197	I36197 Sequence 3
C 8	20	100.0	1641	6	I36196	I36196 Sequence 1
C 9	20	100.0	2224	6	ARI52033	ARI52033 Sequence
C 10	20	100.0	2253	6	A78517	A78517 Sequence 1
C 11	20	100.0	2339	6	A26415	A26415 cDNA fragme
C 12	20	100.0	2394	9	HUMTNFRII	M55994 Human tumor
C 13	20	100.0	3380	11	G26865	G26865 human STS S
C 14	20	100.0	3492	9	S63368	S63368 Homo sapien
C 15	20	100.0	3683	6	AX333705	AX333705 Sequence
C 16	20	100.0	3683	6	AX348016	AX348016 Sequence
C 17	20	100.0	3683	6	AX348018	AX348018 Sequence
C 18	20	100.0	3683	6	AX348020	AX348020 Sequence
C 19	20	100.0	3683	9	HUMNFR	M32315 Human tumor
C 20	20	100.0	122105	2	AL355998	AL355998 Homo sapi
C 21	20	100.0	151498	9	AL357835	AL357835 Human DNA
C 22	20	100.0	187877	2	AC023251	AC023251 Homo sapi
C 23	19	95.0	34	6	A20251	A20251 Oligonucleo
C 24	19	95.0	34	6	I43804	I43804 Sequence 23
C 25	17.4	87.0	129418	2	AC015610	AC015610 Homo sapi
C 26	17.4	87.0	147571	2	AC080177	AC080177 Homo sapi
C 27	17.4	87.0	161739	9	AC105277	AC105277 Homo sapi
C 28	17.4	87.0	173088	2	AC109036	AC109036 Rattus no
C 29	17.4	87.0	173858	2	AC068424	AC068424 Mus muscu
C 30	17.4	87.0	196229	2	AC107667	AC107667 Mus muscu
C 31	16.8	84.0	10387	1	AE013752	AE013752 Yersinia
C 32	16.8	84.0	88203	5	AC097628	AC097628 Takifugu
C 33	16.8	84.0	89044	2	AC022633	AC022633 Homo sapi
C 34	16.8	84.0	110188	2	AC105877	AC105877 Rattus no
C 35	16.8	84.0	127422	8	OSJN00109	AL606693 Oryza sat
C 36	16.8	84.0	135638	1	SYCSLRG	D64005 Synechocyst
C 37	16.8	84.0	142902	2	AC118897	AC118897 Rattus no
C 38	16.8	84.0	156284	2	AC102977	AC102977 Rattus no
C 39	16.8	84.0	162336	9	AC021594	AC021594 Homo sapi
C 40	16.8	84.0	164732	2	AC118946	AC118946 Rattus no
C 41	16.8	84.0	170803	2	AP001641	AP001641 Homo sapi
C 42	16.8	84.0	176525	2	AL845474	AL845474 Mus muscu
C 43	16.8	84.0	182334	2	AP004724	AP004724 Oryza sat
C 44	16.8	84.0	184510	2	AC079059	AC079059 Homo sapi
C 45	16.8	84.0	190066	9	AC010127	AC010127 Homo sapi

ALIGNMENTS

RESULT 1
HSTNFR2S05/c
LOCUS HSTNFR2S05 106 bp DNA linear PRI 31-JUL-1996
DEFINITION Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 5.
ACCESSION U52160
VERSION U52160.1 GI:1469534
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Homo sapiens.
5 of 10
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 106)
Baltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
LePaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and

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/protein_id="BAA89053.1"
/db_xref="GI:6683132"
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40 a 51 c 62 g 46 t
BASE COUNT
ORIGIN

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Oy	1 ACACCACGCTGATGTTC A 20				
Db	81 ACACCACGCTGATGTTC A 62				
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I36350/c	LOCUS	I36350	691 bp	DNA	linear
DEFINITION	Sequence 12 from patent US 5606031.				
ACCESSION	I36350				
VERSION	I36350.1 GI:2086863				

SOURCE	Unknown..
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 691)
TITLE	Lile, J., Kohno, T., Bonam, D. and Rosendahl, M.S. production and purification of biologically active recom-
JOURNAL	neurotrophic protein in bacteria
FEATURES	Patent: US 5606031-A 12 25-FEB-1997; Location/Qualifiers 1. .691
BASE COUNT	160 a 198 c 190 g 143 t
ORIGIN	/organism="unknown"
Query Match	100.0%; Score 20; DB 6; Length 691;
Best Local Similarity	100.0%; Pred. No. 1.5;
Matches	20; Conservative 0; Mismatches 0; Indels 0;

QY	1	ACACCACGCTCTGATGTTTCA	20
Db	553	ACACCACGCTCTGATGTTTCA	534

RESULT 4			
LOCUS	ARI74443/C		
DEFINITION	Sequence 3 from patent US 6306820.	705 bp	DNA
ACCESSION	ARI74443		
VERSION	ARI74443.1	GI:17914763	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
	14base		

BASE COUNT	150 a	244 c	196 g	115 t
ORIGIN				
JOURNAL				
FEATURES				
source	1..705			
	/organism="unknown"			
	Location/Qualifiers			
	Patent: US 6306820-A 3 23-OCT-2001;			
	TNF-mediated diseases			
TITLE	Combination therapy using a TNF binding protein for treating rheumatoid arthritis (patents 1 to 705)			
AUTHORS	Benderle, A.M., Sennello, R.M. and Edwards III, C.K.			

Qy	Query Match	100.0%;	Score 20;	DB 6;	Length 705;	
	Best Local Similarity	100.0%;	Pred. No. 1.5;			
	Matches	20;	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;		
	Db	1	ACACCACGCTCTGATGTTTCA 20			
	Db	415	ACACCACGCTCTGATGTTTCA 396			
RESULT 5	HUMTNFRA/c					
	LOCUS					
	DEFINITION		1080 bp	mRNA	linear	PRI 07-MAR-1995
	ACCESSION					
	VERSION					
	KEYWORDS					
	SOURCE					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	1 (bases 1 to 1080)					
	Heiler, R.A., Song, K., Onasch, M.A., Fischer, W.H., Chang, D. and					
	Ringold, G.M.					
	Complementary DNA cloning of a receptor for tumor necrosis factor					
	and demonstration of a shed form of the receptor					
	Proc. Natl. Acad. Sci. U.S.A. 87 (16), 6151-6155 (1990)					
	90349572					
COMMENT	2166946					
	Draft entry and computer-readable sequence for [1] kindly submitted					
	by R.A.Heiler, 29-JUN-1990.					
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	Db	136	ACACCACGCTCTGATGTTTCA 117			
RESULT 6	AX054825/c					
	LOCUS					
	DEFINITION		1557 bp	DNA	linear	PAT 13-JAN-2001
	Sequence 2 from Patent WO0073481.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	1 (bases 1 to 1557)					
	Burstein, H. and Stepan, A.M.					
	Methods and compositions for lowering the level of tumor necrosis					
	factor (tnf) in tnfr-associated disorders					
	Patent: WO 0073481-A 2 07-DEC-2000;					
	TARGETED GENETICS CORPORATION (US)					
	Location/Qualifiers					
FEATURES	source					
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	/db_xref="taxon:9606"					
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	/codon_start=1					
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	/translation="ARQAAWREGAGLRGREGARAGGNRTPTPASMAPVAVVAALAVGLE					
Qy	Query Match	100.0%;	Score 20;	DB 6;	Length 1557;	
	Best Local Similarity	100.0%;	Pred. No. 1.6;			
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	Indels	0;	Gaps	0;		
	Db	1	ACACCACGCTCTGATGTTTCA 20			
	Db	568	ACACCACGCTCTGATGTTTCA 549			
RESULT 7	I36197/c					
	LOCUS					
	DEFINITION		Sequence 3 from patent US 5605690.			
	ACCESSION					
	VERSION					
	KEYWORDS					
	SOURCE					
ORGANISM	Unknown.					
	Unclassified.					
	1 (bases 1 to 1557)					
	Jacobs, C.A. and Smith, C.A.					
	Methods of lowering active TNF- α levels in mammals using					
	tumor necrosis factor receptor					
	Patent: US 5605690-A 3 25-FEB-1997;					
	Location/Qualifiers					
	source					
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	345 a	526 c	445 g	241 t		
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	Best Local Similarity	100.0%;	Pred. No. 1.6;			
	Matches	20;	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;		
	Db	1	ACACCACGCTCTGATGTTTCA 20			
	Db	568	ACACCACGCTCTGATGTTTCA 549			

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RESULT 8
I36196/c
LOCUS       I36196               1641 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION   Sequence 1 from patent US 5605690.
ACCESSION    I36196
VERSION      I36196.1 GI:2086709
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 1641)
AUTHORS      Jacobs,C.A. and Smith,C.A.
TITLE        Methods of lowering active TNF- $\alpha$  levels in mammals using
              tumor necrosis factor receptor
JOURNAL      Patent: US 5605690-A 1 25-FEB-1997;
FEATURES     Location/Qualifiers
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BASE COUNT   328 a 544 c 502 g 267 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACCACGCTCGATGTTTCA 20
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Db 568 ACACCACGCTCGATGTTTCA 549

RESULT 9
ARI52033/c
LOCUS       ARI52033             2224 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION   Sequence 2 from patent US 6232446.
ACCESSION    ARI52033
VERSION      ARI52033.1 GI:15118083
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 2224)
AUTHORS      Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
TITLE        TNF ligands
JOURNAL      Patent: US 6232446-A 2 15-MAY-2001;
FEATURES     Location/Qualifiers
             source
               1..2224
               /organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACCACGCTCGATGTTTCA 20
|||||
Db 570 ACACCACGCTCGATGTTTCA 551

RESULT 10
A78517/c
LOCUS       A78517             2253 bp      DNA      linear      PAT 19-OCT-1999
DEFINITION   Sequence 1 from Patent EP0585939.
ACCESSION    A78517
VERSION      A78517.1 GI:6090179
KEYWORDS     .
SOURCE       unidentified.
ORGANISM     unidentified.
REFERENCE    1 (bases 1 to 2253)
AUTHORS      Mett,I. and Wallach,D.
TITLE        TNF LIGANDS

JOURNAL      Patent: EP 0585939-A 1 09-MAR-1994;
FEATURES     Location/Qualifiers
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               1..2253
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               CKPCAGTFSNNTSSDTICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
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               GYVNCVIMTVQVRKKPLCLQREAKVPHLPADKARGTQGPQQHLLITAPSSSSLESS
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               HSSQSSQASSTMGDTSSPSEPKDEQVPFSKECAFRSQTETLLGSTEKPLPLGVDPAGMKPS"
BASE COUNT     440 a 709 c 698 g 406 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACCACGCTCGATGTTTCA 20
|||||
Db 570 ACACCACGCTCGATGTTTCA 551

RESULT 11
A26415/c
LOCUS       A26415             2339 bp      DNA      linear      PAT 26-APR-1995
DEFINITION   CDNA fragment for (75kd TNF-BP) tumor necrosis factor binding
ACCESSION    A26415
VERSION      A26415.1 GI:904970
KEYWORDS     .
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
REFERENCE    1 (bases 1 to 2339)
AUTHORS      Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
              Schlaeger,E.J.
TITLE        TNF-binding proteins
JOURNAL      Patent: EP 0417563-A 27 20-MAR-1991;
              F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
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               QPQAPGVEASGAGEARASTGSDSPGSGHTQVNTVCIVNVCSSDHSQSSQAS
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BASE COUNT     494 a 720 c 685 g 440 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2339;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACACCAGTCTGATGTTTCA 20
LOCUS
Db 271 ACACCAGTCTGATGTTTCA 252

RESULT 12
HUMTNFR1I/c
LOCUS
DEFINITION
Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.

ACCESSION
M55994 M38549
VERSION
M55994.1 GI:339757
KEYWORDS
glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.

SOURCE
Human histiocytic lymphoma cell line U937, cDNA to mRNA.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 2394)
AUTHORS
Kohn, T., Brewer, M.T., Baker, S.L., Schwartz, P.E., King, M.W., Hale, K.K., Squires, C.H., Thompson, R.C. and Vannice, J.L.
TITLE
A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)
MEDLINE
91045991
PubMed
2172983

FEATURES
source
Location/Qualifiers
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1..2394
/gene="TNFR1I"
93..1478
/gene="TNFR1I"
/note="603..611 and 669..677 glycosylation site; 861..947 transmembrane domain; 948..1478 cytoplasmic domain; 159,,860 extracellular domain"
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159..1475
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/product="tumor necrosis factor receptor"
/note="putative"
BASE COUNT 484 a 743 c 739 g 428 t

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCAGTCTGATGTTTCA 20
LOCUS
Db 573 ACACCAGTCTGATGTTTCA 554

RESULT 13
G26865/c
LOCUS
DEFINITION
human STS SHGC-31494, sequence tagged site.
ACCESSION
G26865
VERSION
G26865.1 GI:1375115
KEYWORDS
STS; STS sequence; primer; sequence tagged site.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 3380)
AUTHORS
Myers, R.M.
JOURNAL
Unpublished (1995)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: CCCACCACTAGGACTCTGA
Primer B: CACAGAGAGTCAGGACTTGC
STS size: 201
PCR Profile:
Initial Incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from M32315
-- Washington University/Merck EST sequence.

FEATURES
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Location/Qualifiers
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1561..1580
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BASE COUNT 703 a 1029 c 1004 g 644 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCAGTCTGATGTTTCA 20
LOCUS
Db 570 ACACCAGTCTGATGTTTCA 551

RESULT 14
S63368/c
LOCUS
S63368
3492 bp mRNA linear PRI 06-MAR-2001

DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, partial cds.
ACCESSION S63368
VERSION S63368.1 GI:235648
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3492)
Dembic, Z., Loetscher, H., Gubler, U., Pan, Y. C., Lahm, H. W., Gentz, R.,
Brockhaus, M. and Lesslauer, W.
Two human TNF receptors have similar extracellular, but distinct
intracellular, domain sequences
Cytokine 2 (4), 231-237 (1990)
JOURNAL
MEDLINE
PUBMED
REMARK 1966549
GenBank staff at the National Library of Medicine created this
entry [NCBI gibs63368] from the original journal article.
This sequence comes from Figure 1.
FEATURES
Location/Qualifiers
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TGDFALPGLIVGTALGLLIIGVNCVIMTVQKKPLCLQREAKVPHLPADKARGTQ
GPGQHLITAPSSSSSSLESSASALDRRAPTRNQPAQPCVEASGAGEARASTGSSDS
SPGHGTQVNVTCIVNVCSSSDHSSOCSSASTMGDTDSSPSESPKDPQVFPFKKEC
AFRSLETPTLLGSTETKPLPLGVPDAGMKPS"
BASE COUNT 757 a 1031 c 1006 g 598 t
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 373 ACACCACGCTGTGATGTTTCA 354
RESULT 15
AX333705/c
LOCUS AX333705 3683 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 4214 from Patent WO0194629.
ACCESSION AX333705
VERSION AX333705.1 GI:18124424
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 4214 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
Source
1..3683
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 781 a 1098 c 1086 g 718 t

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACACCACGCTGTGATGTTTCA 20
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Db 570 ACACCACGCTGTGATGTTTCA 551
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Job time : 56.6471 secs

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 : Search time 4.80891 Seconds
(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937A-3

Perfect score: 20

Sequence: 1 acaccacgtctgatgtttca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	20	100.0	691	16	AAT05443
C 4	20	100.0	705	19	AAV41549
C 5	20	100.0	705	19	AAV19802
C 6	20	100.0	705	20	AAV81733
C 7	20	100.0	705	21	AAZ45759
C 8	20	100.0	705	21	AAZ45760
C 9	20	100.0	705	21	AAZ45761

C 10	20	100.0	705	21	AAZ45762
C 11	20	100.0	1557	15	AAQ45225
C 12	20	100.0	1557	22	AAC90446
C 13	20	100.0	1640	12	AAQ10990
C 14	20	100.0	1641	14	AAQ49931
C 15	20	100.0	1641	15	AAQ45224
C 16	20	100.0	2224	16	AAQ89544
C 17	20	100.0	2339	12	AAQ10956
C 18	20	100.0	2339	20	AAZ09171
C 19	20	100.0	2339	22	AAH48860
C 20	20	100.0	2393	12	AAQ10907
C 21	20	100.0	2394	22	AAC83951
C 22	20	100.0	3683	24	ABK83997
C 23	20	100.0	3683	24	ABL65877
C 24	20	100.0	3683	24	ABK33465
C 25	20	100.0	3683	24	ABK33466
C 26	20	100.0	3683	24	ABK33467
C 27	19	95.0	34	13	AAQ24451
C 28	15.8	79.0	306	24	ABK76582
C 29	15.8	79.0	474	22	ABA52330
C 30	15.8	79.0	474	22	ABA22125
C 31	15.8	79.0	474	22	AAK00602
C 32	15.8	79.0	474	22	AAK26052
C 33	15.8	79.0	474	22	AAI10680
C 34	15.8	79.0	474	22	AAI19336
C 35	15.8	79.0	474	22	AAI00613
C 36	15.8	79.0	474	24	ABS00635
C 37	15.8	79.0	1712	20	AAZ27501
C 38	15.8	79.0	1712	22	AAS09901
C 39	15.4	77.0	573	24	ABN63733
C 40	15.4	77.0	2382	23	ABL22962
C 41	15.4	77.0	3019	23	ABL09600
C 42	15.4	77.0	3115	22	AAH48125
C 43	15.4	77.0	12724	22	AAK88955
C 44	15.4	77.0	25785	22	AAK78465
C 45	15.2	76.0	416	23	ABV10946

ALIGNMENTS

RESULT 1
AAA49209

ID AAA49209 standard; DNA; 20 BP.

XX AAA49209;

XX 22-NOV-2000 (first entry)

XX Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-CAR.

XX Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;

XX osteoporosis; PCR primer; ss.

XX Homo sapiens.

XX WO200032826-A1.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28403.

XX 30-NOV-1998; 98US-0110268.

XX (UYDR-) UNIV DREXEL.

XX Spotila LD;

XX WPI; 2000-412362/35.

XX Identifying individuals at risk of developing osteoporosis comprises assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene in a DNA sample from an individual -

XX Example 2; Page 11; 21pp; English.
 XX
 CC The present sequence is a PCR primer for the (CA)₁₆ repeat of intron 4 of
 CC the human tumour necrosis factor alpha receptor 2 (TNFR2) gene. It was
 CC thought that this intron might contain a polymorphism related to
 CC osteoporosis. However, it was shown that this was not so. However, exon
 CC 10 contains three polymorphic sites. By determining the genotype of an
 CC individual it is possible to identify those at risk of osteoporosis,
 CC which is characterised by low bone density and fragile bones, later in
 CC life. Those at greatest risk are those who possess allele 1, which is the
 CC rarest allele. This is particularly useful as many cases of osteoporosis
 CC go undetected at present.

XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACACGCTCTGATGTTTCA 20
 |||||
 DB 1 ACACACGCTCTGATGTTTCA 20

RESULT 2
 AAA48203
 ID AAA48203 standard; DNA; 20 BP.

XX AC AAA48203;

XX 15-SEP-2000 (first entry)

XX Reverse PCR primer for detection of TNFRSF1B intron 4 polymorphism.

XX Tumour necrosis factor; TNF; TNF-R2; TNFRSF1B; PCR primer;
 KW tumour necrosis factor receptor superfamily member 1B; human;
 KW cardiovascular disease; coronary artery disease;
 KW non-insulin dependent diabetes mellitus; neuropathy in NIDDM;
 KW essential hypertension; hyperlipidemia; diabetic neuropathy;
 KW vasoprotective; antihypertensive; lipid-lowering;
 KW chromosome lp36.2; D1S2834; ss.

XX Homo sapiens.

OS W0200031293-A1.

XX 02-JUN-2000.

XX 25-NOV-1999; 99WO-AU01050.

XX 25-NOV-1998; 98AU-0007323.

XX (UNSY) UNIV SYDNEY.

XX Morris BJ;

XX WPI; 2000-400096/34.

XX Method for diagnosing a predisposition to a complex polygenic disease
 PT e.g. coronary heart disease, hyperlipidemia and non-insulin-dependent
 PT diabetes mellitus comprises assaying chromosome 1 for a genetic marker

XX Claim 30; Page 3; 50pp; English.

XX A novel method for determining a predisposition in a subject to a
 CC complex polygenic disease involves assaying chromosome 1 for a
 CC genetic marker indicative of a predisposition to the disease. This
 CC method may be used for determining predisposition to cardiovascular
 CC disease, coronary artery disease, non-insulin dependent diabetes
 CC mellitus, neuropathy in NIDDM, essential hypertension, hyperlipidemia
 CC and diabetic neuropathy. The method can be used for testing an

CC individual with a family history or in the early stages of a complex
 CC polygenic disease to ascertain the chance of developing hypertension,
 CC neuropathy or lipid disturbances such as high total cholesterol, high
 CC low density lipoprotein cholesterol, abnormal apolipoprotein AI and
 CC abnormal glycosylated haemoglobin. Once a complex polygenic disease
 CC disposition has been identified the subject can be treated to prevent
 CC or reduce the disease or delay its onset. The genetic marker used
 CC in the method is D1S2834 and includes a CA repeat region in intron
 CC 4 of the tumour necrosis factor receptor superfamily member 1B
 CC (TNFRSF1B) gene. The marker is located at chromosome lp36.2. The
 CC present sequence is the reverse PCR primer used for detection of
 CC the TNFRSF1B intron 4 polymorphism.

XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACACGCTCTGATGTTTCA 20
 |||||
 DB 1 ACACACGCTCTGATGTTTCA 20

RESULT 3
 AAT05443/c
 ID AAT05443 standard; DNA; 691 BP.

XX AC AAT05443;

XX 10-FEB-1996 (first entry)

XX BamTP delta53 nerve growth factor sequence.

XX Nerve growth factor; neurotrophic factor; therapeutic;
 KW protein refolding; NGF; plasmid pT3X1-2; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FT 136..687
 CDS /*tag= a
 FT /*note= "NGF"

XX W09530686-A1.

XX 16-NOV-1995.

XX 02-MAY-1995; 95WO-US05423.

XX 27-JUN-1994; 94US-0266080.

XX 09-MAY-1994; 94US-0240122.

XX (SYNT) SYNTX-SYNERGEN NEUROSCIENCE JOINT VENTU.

XX Bonam D, Kohno T, Lile J, Rosendahl MS;

XX WPI; 1995-404080/51.

XX P-PSDB; AAR77421.

XX Process for bacterial expression of recombinant neurotrophic factor
 PT - useful for promoting the survival and maintaining phenotypic
 PT differentiation of nerve and glial cells.

XX Example 1; Page 36-37; 57pp; English.

XX The synthetic nerve growth factor (NGF) gene isolated from Bam TP
 CC delta 53 plasmid pT3X1-2 is designed to optimize codons for
 CC expression in Escherichia coli as well as create unique sites for
 CC subsequent cloning steps. The recombinant protein is solubilized
 CC and sulfonylated and allowed to refold in the presence of PEG and
 CC urea. Biologically active NGF, used for promoting the survival of
 CC and maintaining the phenotypic differentiation of nerve and glial

CC cells, is isolated and purified. This method breaks incorrectly
 CC formed disulphide bonds and allows refolding of the factor into
 CC the correct tertiary structure required for maximum yield of full
 CC active protein.
 XX

SQ Sequence 691 BP; 160 A; 198 C; 190 G; 143 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 691;
 Best Local Similarity 100.0%; Pred. No. 0.88; Length 691;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCAGCTCTGATGTTTCA 20
 |||||||
 Db 553 ACACCAGCTCTGATGTTTCA 534

RESULT 4

AAV41549/C

ID AAV41549 standard; cDNA; 705 BP.

XX AAV41549;

XX 28-SEP-1998 (first entry)

XX Human soluble tumour necrosis factor receptor type II.

XX Human: tumour necrosis factor; TNF: TNF receptor type II;

KW inflammatory disease; leukaemia; TNF binding protein;

KW anti-inflammatory drug; methotrexate; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..483

FT /*tag a

FT /product= "human soluble TNF receptor type II"

XX WO9824463-A2.

XX 11-JUN-1998.

XX 08-DEC-1997; 97WO-US22733.

XX 09-JUL-1997; 97US-0052023.

XX 06-DEC-1996; 96US-0032587.

XX 23-JAN-1997; 97US-0036355.

XX 07-FEB-1997; 97US-0039315.

XX (AMGE-) AMGEN INC.

XX Bendele AM, Edwards CK, Sennello RM;

XX WPI; 1998-333039/29.

XX P-PSDB; AAW59665.

XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia -

PT by administering tumour necrosis factor binding protein and at least

PT one additional anti-inflammatory drug, e.g. methotrexate

XX Disclosure; Fig 2; 104pp; English.

XX This is the nucleotide sequence of the human tumour necrosis factor

CC receptor type II, used in the method of the invention involving the

CC treatment of acute or chronic inflammatory disease such as leukaemia

CC by administering tumour necrosis factor binding protein and at least

CC one additional anti-inflammatory drug, e.g. methotrexate.

XX Sequence 705 BP; 150 A; 244 C; 196 G; 115 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 705;

Best Local Similarity 100.0%; Pred. No. 0.88;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity 100.0%; Score 20; DB 19; Length 705;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCAGCTCTGATGTTTCA 20
 |||||||
 Db 415 ACACCAGCTCTGATGTTTCA 396

RESULT 5

AAV19802/C

ID AAV19802 standard; cDNA; 705 BP.

XX AAV19802;

XX 29-JUN-1998 (first entry)

XX Tumour necrosis factor inhibitor coding sequence.

XX Soluble tumour necrosis factor receptor; stnfr; TNF-mediated disease;

KW tumour necrosis factor binding protein; autoimmune disease; arthritis;

KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;

KW tumour necrosis factor inhibitor; Alzheimer's disease; TNBP; ss.

XX Homo sapiens.

XX WO9801555-A2.

XX 15-JAN-1998.

XX 09-JUL-1997; 97WO-US12244.

XX 04-MAR-1997; 97US-0039792.

XX 09-JUL-1996; 96US-0021443.

XX 06-DEC-1996; 96US-0032534.

XX 23-JAN-1997; 97US-0037737.

XX 07-FEB-1997; 97US-0039314.

XX (AMGE-) AMGEN INC.

XX Edwards CK, Fisher EF, Kieft GL;

XX WPI; 1998-101052/09.

XX P-PSDB; AAW52270.

XX Truncated and soluble forms of tumour necrosis factor receptor -

PT useful for treating diseases involving factor, e.g. arthritis and

PT adult respiratory distress syndrome

XX Claim 3; Fig 8; 205pp; English.

XX This sequence encodes human tumour necrosis factor inhibitor. The protein

CC was used to make the truncated soluble tumour necrosis factor receptor

CC (stnfr) proteins of the invention. The truncated stnfr proteins and

CC tumour necrosis factor binding proteins (TNBP) are used to treat any

CC TNF-mediated disease, e.g. arthritis, adult respiratory distress

CC syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft

CC rejection, Alzheimer's disease and other autoimmune diseases. Cells

CC transformed with a vector containing DNA encoding the protein may be used

CC for production of recombinant stnfr, which may also be used for measuring

CC the amount of stnfr in samples and to raise antibodies against stnfr.

CC TNBP may also be used in preparation of therapeutic compositions for

CC treating the above diseases. The stnfr proteins are well suited to large

CC scale production (since they lack the deamidation site in region 111-126,

CC so are more stable in vivo); contain fewer disulphide bonds and fewer

CC epitopes, making them less antigenic than full-length proteins.

XX Sequence 705 BP; 150 A; 244 C; 196 G; 115 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 705;

Best Local Similarity 100.0%; Pred. No. 0.88;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity 100.0%; Score 20; DB 19; Length 705;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCAGCTCTGATGTTTCA 20
 |||||||
 Db 415 ACACCAGCTCTGATGTTTCA 396

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RESULT 6
AAV81733/c
ID AAV81733 standard; cDNA; 705 BP.
XX
AC AAV81733;
XX
DT 04-MAR-1999 (first entry)
XX
DE Tumour necrosis inhibitor 40 kDa encoding cDNA.
XX
KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis; ss.
XX
OS Homo sapiens.
XX
PN WO9849305-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US08631.
XX
PR 01-MAY-1997; 97US-0850188.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Wooden S;
XX
DR WPI: 1999-034661/03.
DR P-PSDB: AAW89234.
XX
PT New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
PS Disclosure; Fig 3; 92pp; English.
XX
CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence encodes the TNF inhibitor 40 kDa protein.
XX
SQ Sequence 705 BP; 150 A; 244 C; 196 G; 115 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGTCGTGATGTTTCA 20
DB 415 ACACCACGTCGTGATGTTTCA 396

RESULT 7
AAZ45759/c
ID AAZ45759 standard; DNA; 705 BP.
XX
AC AAZ45759;
XX
DT 25-APR-2000 (first entry)
XX
DE DNA encoding a K120R mutant of soluble p75 TNF receptor.
KW p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
XX

```

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XX AAZ45759;
AC
XX 25-APR-2000 (first entry)
XX
XX DNA encoding a K108R mutant of soluble p75 TNF receptor.
XX
XX p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
XX polyethylene glycol conjugation; PEG conjugation; protein activity; ss.
XX
XX Homo sapiens.
XX OS Synthetic.
XX PN WO9967291-A2.
XX
XX 29-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US13953.
XX
XX 22-JUN-1998; 98US-0102530.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Pettit DK;
XX
XX WPI: 2000-160577/14.
XX P-PSDB: AAY54440.
XX
XX Novel methods for site-specific protein modification by mutagenesis by
XX replacing polyethylene glycol reacting sites -
XX Example 2; Page 28; 36pp; English.
XX
XX The present sequence encodes a N-terminal fragment of a mutant of
XX the soluble tumour necrosis factor (TNF) receptor, where the wild
XX type Lys residue at position 108 is replaced with Arg. Lys108 (and
XX Lys120) make contact between the p75 receptor and ligand. These
XX residues are also potential polyethylene glycol (PEG) conjugation
XX sites. The wild type p75 TNF receptor protein was mutated and conjugated
XX to PEG, using the method of the invention. The specification describes
XX a method for conjugating proteins with PEG to result in
XX PEG-conjugated proteins having little or no reduction in a desired
XX activity. Specifically, one or more amino acid residues that are
XX critical for protein bioactivity and which are capable of reacting
XX with PEG sites are deleted, prior to conjugation of the protein to PEG.
XX The methods provide PEG conjugated proteins that are more homogeneous
XX and present in higher yields. Conjugation does not take place at amino
XX acid residues that are critical to the proteins bioactivity, thus
XX maintaining the activity of the protein. The methods are used to
XX produce PEG conjugated proteins.
XX
XX Query Match 100.0%; Score 20; DB 21; Length 705;
XX Best Local Similarity 100.0%; Pred. No. 0.88;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGTCGTGATGTTTCA 20
DB 415 ACACCACGTCGTGATGTTTCA 396

RESULT 8
AAZ45760/c
ID AAZ45760 standard; DNA; 705 BP.
XX
XX AAZ45760;
XX
XX 25-APR-2000 (first entry)
XX
XX DNA encoding a K120R mutant of soluble p75 TNF receptor.
XX
XX p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
XX

```


KW polyethylene glycol conjugation; PEG conjugation; protein activity; ss.
XX Homo sapiens.
OS Synthetic.
XX WO9967291-A2.
XX 29-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US13953.
XX 22-JUN-1998; 98US-0102530.
XX (IMMV) IMMUNEX CORP.
XX Pettit DK;
XX
XX WPI; 2000-160577/14.
XX P-PSDB; AAY54451.
XX
XX Novel methods for site-specific protein modification by mutagenesis by
PT replacing polyethylene glycol reacting sites -
XX Example 2; Page 30-31; 36pp; English.
XX
XX The present sequence encodes a N-terminal fragment of a mutant of
CC the soluble tumour necrosis factor (TNF) receptor, where the wild
CC type Lys residue at position 120 is replaced with Arg. Lys120 (and
CC Lys108) make contact between the p75 receptor and ligand. These
CC residues are also potential polyethylene glycol (PEG) conjugation
CC sites. The wild type p75 TNF receptor protein was mutated and conjugated
CC to PEG, using the method of the invention. The specification describes
CC a method for conjugating proteins with PEG to result in
CC PEG-conjugated proteins having little or no reduction in a desired
CC activity. Specifically, one or more amino acid residues that are
CC critical for protein bioactivity and which are capable of reacting
CC with PEG sites are deleted, prior to conjugation of the protein to PEG.
CC The methods provide PEG conjugated proteins that are more homogeneous
CC and present in higher yields. Conjugation does not take place at amino
CC acid residues that are critical to the proteins bioactivity, thus
CC maintaining the activity of the protein. The methods are used to
CC produce PEG conjugated proteins.
XX
SQ Sequence 705 BP; 150 A; 244 C; 195 G; 116 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACCACGCTGATGTTTCA 20
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 9
ID AA245761/C
XX AA245761 standard; DNA; 705 BP.
XX AA245761;
XX
XX 25-APR-2000 (first entry)
XX
XX DNA encoding a K108R/K120R mutant of soluble p75 TNF receptor.
XX
XX p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
KW polyethylene glycol conjugation; PEG conjugation; protein activity; ss.
XX Homo sapiens.
OS Synthetic.
XX WO9967291-A2.
XX 29-DEC-1999.

XX 18-JUN-1999; 99WO-US13953.
XX 22-JUN-1998; 98US-0102530.
XX (IMMV) IMMUNEX CORP.
XX Pettit DK;
XX
XX WPI; 2000-160577/14.
XX P-PSDB; AAY54442.
XX
XX Novel methods for site-specific protein modification by mutagenesis by
PT replacing polyethylene glycol reacting sites -
XX Example 2; Page 32-33; 36pp; English.
XX
XX The present sequence encodes a N-terminal fragment of a mutant of the
CC soluble tumour necrosis factor (TNF) receptor, where the wild type Lys
CC residues at positions 108 and 120 are replaced with Arg. Lys120 and
CC Lys108 make contact between the p75 receptor and ligand. These
CC residues are also potential polyethylene glycol (PEG) conjugation
CC sites. The wild type p75 TNF receptor protein was mutated and conjugated
CC to PEG, using the method of the invention. The specification describes
CC a method for conjugating proteins with PEG to result in
CC PEG-conjugated proteins having little or no reduction in a desired
CC activity. Specifically, one or more amino acid residues that are
CC critical for protein bioactivity and which are capable of reacting
CC with PEG sites are deleted, prior to conjugation of the protein to PEG.
CC The methods provide PEG conjugated proteins that are more homogeneous
CC and present in higher yields. Conjugation does not take place at amino
CC acid residues that are critical to the proteins bioactivity, thus
CC maintaining the activity of the protein. The methods are used to
CC produce PEG conjugated proteins.
XX
SQ Sequence 705 BP; 149 A; 244 C; 196 G; 116 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACCACGCTGATGTTTCA 20
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 10
ID AA245762/C
XX AA245762 standard; DNA; 705 BP.
XX AA245762;
XX
XX 25-APR-2000 (first entry)
XX
XX Wild type N-terminal fragment of the soluble p75 TNF receptor DNA.
XX
XX p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
KW polyethylene glycol conjugation; PEG conjugation; protein activity; ss.
XX Homo sapiens.
OS
XX WO9967291-A2.
XX
XX 29-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US13953.
XX 22-JUN-1998; 98US-0102530.
XX (IMMV) IMMUNEX CORP.
XX Pettit DK;
XX

DR WPI: 2000-160577/14.
 DR P-PSDB; AAY54443.
 XX
 PT Novel methods for site-specific protein modification by mutagenesis by
 PT replacing polyethylene glycol reacting sites -
 XX
 PS Example 2; Page 34-35; 36pp; English.
 XX
 CC The present sequence encodes a N-terminal fragment of the soluble
 CC tumour necrosis factor (TNF) receptor. The wild type Lys residues at
 CC positions 108 and 120 are replaced with Arg (see AAY54441-42). Lys120
 CC and Lys108 make contact between the p75 receptor and ligand. These
 CC residues are also potential polyethylene glycol (PEG) conjugation
 CC sites. The wild type p75 TNF receptor protein was mutated and conjugated
 CC to PEG, using the method of the invention. The specification describes
 CC a method for conjugating proteins with PEG to result in
 CC PEG-conjugated proteins having little or no reduction in a desired
 CC activity. Specifically, one or more amino acid residues that are
 CC critical for protein bioactivity and which are capable of reacting
 CC with PEG sites are deleted, prior to conjugation of the protein to PEG.
 CC The methods provide PEG conjugated proteins that are more homogeneous
 CC and present in higher yields. Conjugation does not take place at amino
 CC acid residues that are critical to the proteins bioactivity, thus
 CC maintaining the activity of the protein. The methods are used to
 CC produce PEG conjugated proteins.
 XX
 SQ Sequence 705 BP; 151 A; 244 C; 194 G; 116 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 705;
 Best Local Similarity 100.0%; Pred. No. 0.88;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
 |||||
 DB 415 ACACCACGCTGATGTTTCA 396

RESULT 11
 AAQ45225/C
 ID AAQ45225 standard; cDNA; 1557 BP.
 XX
 AC AAQ45225;
 XX
 DT 07-OCT-1994 (first entry)
 XX
 DE Sequence encoding a recombinant human tumour necrosis factor receptor
 DE TNFR/fc fusion protein.
 XX
 KW Tumour necrosis factor receptor; chimeric antibody molecule;
 KW Immunoglobulin; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..1554
 FT /*tag- a
 XX
 PN WO9406476-A.
 XX
 PD 31-MAR-1994.
 XX
 PF 14-SEP-1993; 93WO-US08666.
 XX
 PR 15-SEP-1992; 92US-0946236.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Jacobs CA, Smith CA;
 XX
 XX WPI; 1994-118172/14.
 DR P-PSDB; AAR51003.
 XX
 PT Treating TNF mediated inflammatory diseases with TNF antagonist -

PT esp. soluble form of TNF receptor, opt. as fusion protein with
 PT human immunoglobulin Fc region, esp. for treating arthritis
 XX
 PS Disclosure; Page 32-34; 47pp; English.
 XX
 CC AAQ45224 is cDNA from clone 1 of library WI-26 V44 of human fibroblast
 CC cell line WI-26 V44. The mature full-length TNFR1 is a glycoprotein
 CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
 CC TNFR1 was described in Smith et al., Science 248:1019,1990. Clone 1
 CC is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A
 CC recombinant chimeric antibody may be produced having TNFR sequences
 CC substituted for the variable domains of either or both of the
 CC immunoglobulin molecule heavy and light chains and having
 CC unmodified constant region domains. A specific example of a TNFR/Fc
 CC fusion protein is given in AAQ45225/R51003. The rhu TNFR:Fc fusion
 CC gene was created by ligating the following fragments into a cloning
 CC vector: 1) an 867 bp Asp718-Pvu2 fragment from pCAV/NOT-TNFR (ATCC
 CC 68088) contg. the cDNA encoding the truncated TNFR. 2) a 700 bp
 CC Styl-SpeI fragment from plasmid pIXV498 coding for 232 AAs of the
 CC Fc portion of human IgG1. Plasmid pIXV498 is a yeast expression
 CC vector contg. the Fc fragment of human IgG1. 3) An oligo linker, to
 CC fuse the truncated TNFR with the human IgG1 Fc fragment. This
 CC linker was created by PCR using primer AAQ45226, which encodes the 3'
 CC end of the truncated TNF receptor and the 5' end of human IgG1 and
 CC primer AAQ45227, which is an antisense sequence encoding bps 257-237
 CC of human IgG1.
 XX
 SQ Sequence 1557 BP; 345 A; 524 C; 445 G; 243 T; 0 other;

Query Match 100.0%; Score 20; DB 15; Length 1557;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
 |||||
 DB 568 ACACCACGCTGATGTTTCA 549

RESULT 12
 AAC90446/C
 ID AAC90446 standard; cDNA; 1557 BP.
 XX
 AC AAC90446;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE TNFR:Fc fusion protein coding sequence.
 XX
 KW Antinflammatory; antiarthritic; gene therapy; inflammatory disorder;
 KW Tumour Necrosis Factor receptor; TNFR; IgG1 Fc domain; asthma;
 KW rheumatoid arthritis; Crohn's disease; congestive heart failure; ss.
 XX
 OS Rattus sp.
 XX
 PN WO200073481-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14586.
 XX
 PR 28-MAY-1999; 99US-0150688.
 XX
 PA (TARG-) TARGETED GENETICS CORP.
 XX
 PI Burstein H, Stepan AM;
 XX
 DR WPI; 2001-061552/07.
 DR P-PSDB; AAB50080.
 XX
 XX Recombinant adeno-associated virus vector, useful for palliating tumor
 PT necrosis factor associated disorder, comprises polynucleotide which
 PT encodes fusion polypeptide comprising tumor necrosis factor receptor -

PS Example 1; Fig 2; 90pp; English.

CC The present invention relates to a recombinant adeno-associated virus
 CC (rAAV) vector comprising a polynucleotide (the present sequence) which
 CC encodes a fusion protein comprising an extracellular domain of Tumour
 CC Necrosis Factor receptor (TNFR) and a constant domain (Fc) of IgG1
 CC molecule. The vector of the present invention is useful for reducing TNF
 CC levels, for reducing an inflammatory response which occurs in a
 CC connective tissue and for palliating a TNF-associated disorder such as
 CC inflammatory disorders e.g. rheumatoid arthritis, Crohn's disease, asthma
 CC and congestive heart failure.

XX SQ Sequence 1557 BP; 345 A; 526 C; 445 G; 241 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 1557;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACCACGCTCGATGTTTCA 20

|||||

Db 568 ACACCACGCTCGATGTTTCA 549

RESULT 13

AAQ10990/c

ID AAQ10990 standard; cDNA to mRNA; 1640 BP.

XX AC AAQ10990;

DT 24-MAY-1991 (first entry)

XX Partial sequence of hTNF-R clone 1.

DE Tumour necrosis factor receptor; immune response; inflammation;
 KW cachexia; septic shock; ss.

XX Homo sapiens.

Key Location/Qualifiers

FT CDS 88..1473

FT /*tag= a

FT mat_peptide 154..1470

FT /*tag= b

FT sig_peptide 88..153

FT /*tag= c

XX EP418014-A.

XX 20-MAR-1991.

XX 10-SEP-1990; 90EP-0309875.

XX 10-MAY-1990; 90US-0523635.

PR 11-SEP-1989; 89US-0405370.

PR 13-OCT-1989; 89US-0421417.

XX (IMMU-) IMMUNEX CORP.

XX Smith CA, Goodwin RG, Beckmann PW;

XX WPI: 1991-082230/12.

XX P-PSDB: AAR11141.

XX New tumour necrosis factor -alpha and -beta receptors - and DNA
 PT encoding these used to regulate immune responses in treatment of
 PT cachexia, septic shock or side-effects of cytokine therapy.

XX Claim 1; Fig 2; 41pp; English.

XX The sequence was obtd. from a clone isolated from library prepd.
 CC from a human fibroblast cell line, WI-26 V44 (ATCC CCL 95.1).
 CC The clone is deposited as Accession No. 68088 under the name
 CC pCAV/NOT-TNF-R. The DNA can be truncatd to produce sequences which

CC express soluble receptor comprising residues 1-235, 1-185 or 1-163
 CC of the protein.
 CC See also AAQ10991.

XX SQ Sequence 1640 BP; 328 A; 543 C; 502 G; 267 T; 0 other;

Query Match 100.0%; Score 20; DB 12; Length 1640;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACCACGCTCGATGTTTCA 20

|||||

Db 568 ACACCACGCTCGATGTTTCA 549

RESULT 14

AAQ49931/c

ID AAQ49931 standard; cDNA to mRNA; 1641 BP.

XX AC AAQ49931;

XX 29-APR-1994 (first entry)

XX TNF-R cDNA.

XX Homo sapiens.

KW IL-1R; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
 KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
 KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
 KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
 KW graft verses host disease; sepsis; inflammation; allergy;
 KW autoimmune dysfunction; ss.

XX Homo sapiens.

Key Location/Qualifiers

FT CDS 88..1473

FT /*tag= a

FT sig_peptide 88..153

FT /*tag= b

FT mat_peptide 154..1470

FT /*tag= c

XX WO9319777-A.

XX 14-OCT-1993.

XX 26-MAR-1993; 93WO-US02938.

XX 30-MAR-1992; 92US-0860710.

XX (IMMV) IMMUNEX CORP.

XX Smith CA;

XX WPI: 1993-336592/42.

XX P-PSDB: AAR42058.

XX New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.

XX Disclosure; Fig 2; 85pp; English.

XX The sequences given in AAQ49931-32 encode human tumour necrosis factor
 CC receptor (TNF-R) and the sequences in AAQ49933-34 encode human
 CC interleukin-1 receptor (IL-1R). These sequences were used in the
 CC production of a fusion protein which conformed to one of the
 CC formulae:
 CC TNF-R-linker-TNF-R-linker-IL-1R
 CC IL-1R-linker-TNF-R-linker-TNF-R or
 CC TNF-R-linker-TNF-R

XX The linker may comprise 5-100 amino acids selected from Gly, Asp,

CC Ser, Thr and Ala. These linkers separate the individual moieties
CC by such a distance that each component of the fusion protein is
CC capable of folding into the secondary or tertiary structure required
CC for its biological activity. These fusion proteins may be used in
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC particularly in conditions in which both TNF and IL-1 play a causative
CC role. They may be used to treat cachexia, rheumatoid arthritis,
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC cerebral malaria, allograft and xenograft rejection in graft verses
CC host disease, sepsis, septic shock, inflammation, allergies and
CC autoimmune dysfunctions.

XX
SQ Sequence 1641 BP; 328 A; 544 C; 502 G; 267 T; 0 other;
Query Match 100.0%; Score 20; DB 14; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
IIIIIIIIIIIIIIIIIIII
DB 568 ACACCACGCTCTGATGTTTCA 549

RESULT 15
AAQ45224/c
ID AAQ45224 standard; cDNA; 1641 BP.
XX AC AAQ45224;
XX AC AAQ45224;
DT 07-OCT-1994 (first entry)
XX
XX Sequence encoding human tumour necrosis factor receptor type I
DE (TNFRI).
DE
KW Tumour necrosis factor receptor; type I; TNFRI; arthritis therapy; ss.
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT mat_peptide 154..1470
FT /*tag= a
FT sig_peptide 88..153
FT /*tag= b

XX W09406476-A.
XX
XX 31-MAR-1994.
XX
XX 14-SEP-1993; 93WO-US08666.
XX
XX 15-SEP-1992; 92US-0946236.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Jacobs CA, Smith CA;
XX
XX WPI; 1994-118172/14.
XX P-PSDB; AAR51002.
XX
XX Treating TNF mediated inflammatory diseases with TNF antagonist -
PT esp. soluble form of TNF receptor, opt. as fusion protein with
PT human immunoglobulin Fc region, esp. for treating arthritis
XX
XX Disclosure: Page 28-30; 47pp; English.
XX
XX AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
CC cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein
CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
CC TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1
CC is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The
CC preferred TNFRs of the present invention are soluble forms of TNFRI
CC and TNFRII having at least 20 AAs. Soluble TNFR constructs are
CC devoid of a transmembrane region but retain the ability to bind TNF.

CC Examples of soluble TNFRs are huTNFRdelta235, huTNFRdelta185 and
CC huTNFRdelta163 which encode respectively AAs 1-235,1-185 and 1-163
CC of AAR51002. An equivalent soluble TNFR is huTNFRdelta163 wherein x
CC is selected from any one of AAs 163-235 of AAR51002.
XX
SQ Sequence 1641 BP; 328 A; 526 C; 520 G; 267 T; 0 other;
Query Match 100.0%; Score 20; DB 15; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
IIIIIIIIIIIIIIIIIIII
DB 568 ACACCACGCTCTGATGTTTCA 549

Search completed: December 5, 2002, 23:30:00
Job time : 8.80891 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 ; Search time 38.2783 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937A-3

Perfect score: 20

Sequence: 1 acaccacgtctgatgtttca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	20	100.0	268	9	AA362428
c 2	20	100.0	419	12	BF764027
c 3	20	100.0	485	10	AW856055
c 4	20	100.0	652	12	BF204631
c 5	20	100.0	741	12	BG828205
c 6	20	100.0	777	10	BE299738

c	7	20	100.0	781	13	BI115162
c	8	20	100.0	807	13	BI822108
c	9	20	100.0	982	12	BF310740
c	10	20	100.0	1177	12	BG109353
c	11	20	100.0	2291	11	BC011844
c	12	18	90.0	680	9	AJ272769
c	13	17.4	87.0	1097	14	BQ924155
c	14	17	85.0	301	17	AO816262
c	15	17	85.0	780	12	BF203997
c	16	16.8	84.0	220	9	AU265128
c	17	16.8	84.0	323	9	AU264082
c	18	16.8	84.0	335	9	AU264081
c	19	16.8	84.0	391	9	AU268690
c	20	16.8	84.0	405	9	AU265129
c	21	16.8	84.0	406	9	AU262031
c	22	16.8	84.0	414	9	AU262158
c	23	16.8	84.0	417	9	AU262205
c	24	16.8	84.0	419	9	AU268689
c	25	16.8	84.0	425	13	BJ434049
c	26	16.8	84.0	426	9	AU269353
c	27	16.8	84.0	427	9	AU269417
c	28	16.8	84.0	431	9	AU269352
c	29	16.8	84.0	432	9	AU266818
c	30	16.8	84.0	434	9	AU262912
c	31	16.8	84.0	437	9	AU265521
c	32	16.8	84.0	443	9	AU269416
c	33	16.8	84.0	444	9	AU266547
c	34	16.8	84.0	446	13	BJ415788
c	35	16.8	84.0	446	9	AU269122
c	36	16.8	84.0	487	17	AQ327710
c	37	16.8	84.0	511	17	AQ485844
c	38	16.8	84.0	563	10	AW880527
c	39	16.8	84.0	947	12	BF980620
c	40	16.8	84.0	976	12	BF243262
c	41	16.4	82.0	372	17	FR0044026
c	42	16.4	82.0	386	17	FR0044052
c	43	16.4	82.0	430	17	AZ076324
c	44	16.4	82.0	567	10	BE430928
c	45	16.4	82.0	581	9	AA232311

ALIGNMENTS

RESULT 1
AA362428/c

LOCUS AA362428

DEFINITION EST72059 Monocytes, stimulated

ACCESSION AA362428

VERSION AA362428.1

KEYWORDS EST

SOURCE human

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 268)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A.,

Gelley,J.C., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,

Moreno-Palmer,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudke,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,

Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,

Kunsch,C., Hwang,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,

Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon

,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

268 bp mRNA linear EST 21-APR-1997
tumor necrosis factor receptor 2, mRNA sequence.

BI115162 602863085
BF822108 603039994
BF310740 601895733
BG109353 602280404
BC011844 Homo sapi
AJ272769 AJ272769
BQ924155 AGENCOURT
AO816262 HS_5498.A
BF203997 601869116
AU265128 AU265128
AU264082 AU264082
AU264081 AU264081
AU268690 AU268690
AU265129 AU265129
AU262031 AU262031
AU262158 AU262158
AU262205 AU262205
AU268689 AU268689
BJ434049 BJ434049
AU269353 AU269353
AU269417 AU269417
AU269352 AU269352
AU266818 AU266818
AU262912 AU262912
AU265521 AU265521
AU269416 AU269416
AU266547 AU266547
BJ415788 BJ415788
AU269122 AU269122
AQ327710 nbx0041J
AQ485844 RPC1-11-2
AW880527 QVO-OT003
BF980620 602303831
BF243262 601877195
AL131518 Fugu rubr
AL131544 Fugu rubr
AZ076324 RPC1-23-3
BE430928 SUN008.F0
AA232311 zr23all.s

TITLE
JOURNAL
MEDLINE
COMMENT

Venter, J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl.), 3-174 (1995)
 96026280
 Other_ESTs: THCL166535
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source

BASE COUNT 65 a 96 c 62 g 43 t 2 others
ORIGIN

1. .268
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):166699"
 /db_xref="taxon:9606"
 /clone_lib="Monocytes, stimulated II"
 /cell_type="monocyte"
 /dev_stage="adult"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 EcoRI"

Query Match 100.0%; Score 20; DB 9; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
 |||||||||||||||||||
Db 31 ACACCACGCTCTGATGTTTCA 12

RESULT 2
BF764027

LOCUS BF764027 419 bp mRNA linear EST 12-JAN-2001
DEFINITION IL2-CS0048-301000-198-F06 CS0048 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF764027
VERSION BF764027.1 GI:12111927
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 419)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-CS0048-301000-198-F06&t3=2000-10-30&t4=1>)

FEATURES
 source

Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 418.
 Locat on/Qualifiers
 1. .419
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CS0048"
 /dev_stage="Adult"

/note="Organ: colon_est; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 75 a 122 c 136 g 86 t
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 419;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
 |||||||||||||||||||
Db 227 ACACCACGCTCTGATGTTTCA 246

RESULT 3
AW856055/c

LOCUS AW856055/c 485 bp mRNA linear EST 19-MAY-2000
DEFINITION RC1-CT0286-060200-015-d07 CT0286 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW856055
VERSION AW856055.1 GI:7951748
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 485)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC1-CT0286-060200-015-d07&t3=2000-02-06&t4=1>)

Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence stop: 485.
 Location/Qualifiers
 1. .485
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0286"
 /dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 116 a 153 c 122 g 94 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
|||||
Db 41 ACACCACGCTCTGATGTTTCA 22

RESULT 4
BF204631/c

LOCUS 601867053F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109677 5',
DEFINITION mRNA sequence.
ACCESSION BF204631
VERSION BF204631.1 GI:11098217
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 652)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM994 row: j column: 14
High quality sequence stop: 650.
FEATURES
Location/Qualifiers
1. .652

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4109677"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected by for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 121 a 215 c 215 g 101 t
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 652;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
|||||
Db 471 ACACCACGCTCTGATGTTTCA 452

RESULT 5
BG828205/c

LOCUS 60275359F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4905910 5',
DEFINITION mRNA sequence.
ACCESSION BG828205
VERSION BG828205.1 GI:14175780
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1808 row: b column: 23
High quality sequence stop: 741.
FEATURES
Location/Qualifiers
1. .741

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4905910"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected by for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 141 a 261 c 228 g 111 t
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 741;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
|||||
Db 471 ACACCACGCTCTGATGTTTCA 452

RESULT 6
BE299738/c

LOCUS 600944393F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960374 5',
DEFINITION mRNA sequence.
ACCESSION BE299738
VERSION BE299738.1 GI:9183486
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 777)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM53 row: j column: 23
 High quality sequence stop: 776.
 Location/Qualifiers

FEATURES

source

1..777
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2960374"
 /clone_lib="NIH_MGC_17"
 /tissue_type="rhabdomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
 Site_2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 145 a 260 c 232 g 140 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 777;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACACCACGCTCTGATGTTTCA 20
 ||||||||||||||||||
 Db 460 ACACCACGCTCTGATGTTTCA 441

RESULT 7

BI115162/c
 LOCUS 781 bp mRNA linear EST 26-JUN-2001
 DEFINITION 602863085F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:5022068 5',
 mRNA sequence.
 ACCESSION BI115162
 VERSION BI115162.1 GI:145666063
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 781)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue procurement: ATCC

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1841 row: j column: 21
 High quality sequence stop: 744.
 Location/Qualifiers

FEATURES

source

1..781
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5022068"
 /clone_lib="NIH_MGC_17"
 /tissue_type="rhabdomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
 Site_2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 156 a 253 c 245 g 127 t
 ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 781;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
 ||||||||||||||||||
 Db 470 ACACCACGCTCTGATGTTTCA 451

RESULT 8

BI822108/c
 LOCUS 807 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603039994F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181070 5',
 mRNA sequence.
 ACCESSION BI822108
 VERSION BI822108.1 GI:15933658
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 807)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM11451 row: k column: 23
 High quality sequence stop: 801.

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM11451 row: k column: 23
 High quality sequence stop: 801.

FEATURES

source

1..807
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5181070"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research genetics tracking code
 021. Note: this is a NIH_MGC Library."
 BASE COUNT 157 a 283 c 240 g 127 t
 ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 807;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
 ||||||||||||||||||
 Db 543 ACACCACGCTCTGATGTTTCA 524

RESULT 9


```

BF310740/c
LOCUS      BF310740      982 bp      mRNA      linear      EST 21-NOV-2000
DEFINITION 601895733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124840 5',
            mRNA sequence.
ACCESSION  BF310740
VERSION     BF310740.1 GI:11258352
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 982)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: L1CM1012 row: b column: 09
            High quality sequence stop: 691.
FEATURES   Location/Qualifiers
            source          1..982
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:4124840"
                        /clone_lib="NIH_MGC_19"
                        /tissue_type="neuroblastoma"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                        EcoRI; cDNA made by oligo-dT priming. Directionally
                        cloned into EcoRI/XhoI sites using the following 5'
                        adaptor: GGCACGAG(G). Library constructed by Ling Hong
                        in the laboratory of Gerald M. Rubin (University of
                        California, Berkeley) using ZAP-cDNA synthesis kit
                        (Stratagene) and Superscript II RT (Life Technologies).
                        Note: this is a NIH_MGC Library."
BASE COUNT 222 a 246 c 316 g 198 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 982;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
    |||||
DB 495 ACACCACGCTGATGTTTCA 476

RESULT 10
BG109353/c
LOCUS      BG109353      1177 bp      mRNA      linear      EST 30-JAN-2001
DEFINITION 602280404F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368025 5',
            mRNA sequence.
ACCESSION  BG109353
VERSION     BG109353.1 GI:12602859
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1177)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.

```

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10021 row: g column: 02
High quality sequence stop: 705.
FEATURES   Location/Qualifiers
            source          1..1177
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:4368025"
                        /clone_lib="NIH_MGC_86"
                        /tissue_type="osteosarcoma, cell line"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                        Average insert size 1.533 kb. Library enriched for
                        full-length clones and constructed by Life Technologies.
                        Note: this is a NIH_MGC Library."
BASE COUNT 293 a 365 c 353 g 166 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 1177;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
    |||||
DB 442 ACACCACGCTGATGTTTCA 423

RESULT 11
BC011844/c
LOCUS      BC011844      2291 bp      mRNA      linear      HTC 02-AUG-2001
DEFINITION Homo sapiens, Similar to tumor necrosis factor receptor
            superfamily, member 1B, clone IMAGE:4111730, mRNA.
ACCESSION  BC011844
VERSION     BC011844.1 GI:15080140
KEYWORDS    HTC.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2291)
AUTHORS    Strausberg, R.
TITLE      Direct Submission
JOURNAL    Submitted (30-JUL-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact:
            nisc_mgc@nhgri.nih.gov
            Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
            Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
            Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
            Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
            McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
            Tngson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
            Zhang, L.-H. and Green, E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 28 Row: 1 Column: 15

```

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
 This clone has the following problem: incomplete processing.

```

FEATURES             source
  source
    1..2291
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:4111730"
      /tissue_type="Muscle, rhabdomyosarcoma"
      /clone_lib="NIH_MGC_17"
      /lab_host="DH10B-R"
      /note="Vector: pOTB7"
BASE COUNT          461 a 708 c 713 g 409 t
ORIGIN
Query Match          100.0%; Score 20; DB 11; Length 2291;
Best Local Similarity 100.0%; Pred. NO. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTCGATGTTTCA 20
|||||
Db 479 ACACCACGCTCGATGTTTCA 460

RESULT 12
AJ272769/c           680 bp mRNA linear EST 29-DEC-1999
LOCUS
DEFINITION
  cDNA clone Ma#92, mRNA sequence.
ACCESSION
  AJ272769
VERSION
  AJ272769.1 GI:6432142
KEYWORDS
  EST.
SOURCE
  Metarhizium anisopliae.
  ORGANISM
    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
    Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
    Metarhizium.
  REFERENCE
    1 (bases 1 to 680)
    Screen, S.E., Mathur, P. and St. Leger, R.J.
  AUTHORS
    EST analysis of the insect pathogenic fungus Metarhizium anisopliae
  TITLE
    Unpublished (1999)
  JOURNAL
    Contact: Screen SE
  COMMENT
    Entomology
    University of Maryland
    4112 Plant Sciences Building, College Park, MD 20742, USA.
FEATURES             source
  source
    1..680
      /organism="Metarhizium anisopliae"
      /strain="ARSEF 2575"
      /db_xref="taxon:5530"
      /clone="Ma#92"
      /clone_lib="Metarhizium anisopliae ARSEF 2575"
      /note="Vector: Unizap; Metarhizium anisopliae was grown on
      insect cuticle for 24 hours. A cDNA library was
      constructed in the unidirectional Lambda vector, Unizap"
BASE COUNT          157 a 177 c 183 g 159 t
ORIGIN
Query Match          90.0%; Score 18; DB 9; Length 680;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCACGCTCGATGTTTC 19
|||||
Db 160 CACCACGCTCGATGTTTC 143

RESULT 13
BQ924155/c          1097 bp mRNA linear EST 20-AUG-2002
LOCUS
DEFINITION
  AGENCOURT_8877927 Lupski_sciatic_nerve Homo sapiens cDNA clone
  IMAGE:6198614 5', mRNA sequence.

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```

ACCESSION            BQ924155
VERSION              BQ924155.1 GI:22339186
KEYWORDS
SOURCE
  human.
  ORGANISM
    Homo sapiens
  REFERENCE
    1 (bases 1 to 1097)
    NIH-MGC http://mgi.nci.nih.gov/.
  AUTHORS
    National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE
    Unpublished (1999)
  JOURNAL
    Contact: Robert Strausberg, Ph.D.
  COMMENT
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Dr. James R. Lupski
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM13610 row: i column: 15
    High quality sequence stop: 492.
FEATURES             source
  source
    1..1097
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:6198614"
      /clone_lib="Lupski_sciatic_nerve"
      /sex="male"
      /tissue_type="sciatic nerve"
      /dev_stage="adult, 70 yr"
      /lab_host="DH10B"
      /note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
      NotI; Site_2: SalI; cDNA made by oligo-dT priming.
      Directionally cloned using the following adaptors:
      5'-TCGACCCACGCGTCCG-3' and
      5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
      1 kb for average insert length 1.87 kb. This is a primary
      library, non-amplified. Library constructed by Life
      Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
      College of Medicine) and is available through Life
      Technologies."
BASE COUNT          183 a 351 c 427 g 136 t
ORIGIN
Query Match          87.0%; Score 17.4; DB 14; Length 1097;
Best Local Similarity 94.7%; Pred. NO. 3.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CACCACGCTCGATGTTTCA 20
|||||
Db 562 CACCACGCTCGATGTTTCA 544

RESULT 14
AQ816262/c          301 bp DNA linear GSS 26-AUG-1999
LOCUS
DEFINITION
  genomic clone Plate-1074 Col-2 Row=I, DNA sequence.
ACCESSION
  AQ816262
VERSION
  AQ816262.1 GI:5778655
KEYWORDS
  GSS.
SOURCE
  human.
  ORGANISM
    Homo sapiens
  REFERENCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
    1 (bases 1 to 301)
    Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
    Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
    Hood, L.
  TITLE
    Sequence-tagged connectors: A sequence approach to mapping and
    scanning the human genome
  JOURNAL
    Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

```

MEDLINE COMMENT

99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (<http://www.hsc.washington.edu>) Plate: 1074 row: 1 column: 2

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 301.

Location/Qualifiers

1..301

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="plate:1074 Col=2 Row=1"

/clone.lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

62 c 73 g 64 t

BASE COUNT ORIGIN

Query Match 85.0%; Score 17; DB 17; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCACGCTCTGATGTT 18
|||||

Db 121 CACCACGCTCTGATGTT 105

RESULT 15

BF203997/c

LOCUS 601869116F1 NIH_MGC_17 780 bp mRNA linear EST 06-NOV-2000
DEFINITION 601869116F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111730 5',
mRNA sequence.

ACCESSION BF203997

VERSION BF203997.1 GI:11097583

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 780)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM999 row: P column: 03

High quality sequence stop: 679.

Location/Qualifiers

1..780

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4111730"

FEATURES

source

/clone.lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected by
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 161 a 214 c 254 g 150 t 1 others
ORIGIN

Query Match 85.0%; Score 17; DB 12; Length 780;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTT 17
|||||

Db 506 ACACCACGCTCTGATGTT 490

Search completed: December 6, 2002, 04:54:20

Job time : 50.2783 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 ; Search time 1.03896 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-3
Perfect score: 20
Sequence: 1 acaccagctctgatgtttca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	36	6	Patent No. 5395760
C 2	20	100.0	691	1	US-08-266-080B-12
C 3	20	100.0	691	5	PCT-US95-05423-12
C 4	20	100.0	705	4	US-09-326-394-3
C 5	20	100.0	705	4	US-09-580-235-1
C 6	20	100.0	705	4	US-09-580-235-3
C 7	20	100.0	705	4	US-09-580-235-5
C 8	20	100.0	705	4	US-09-580-235-7
C 9	20	100.0	705	4	US-09-580-181-1
C 10	20	100.0	705	4	US-09-580-181-3
C 11	20	100.0	705	4	US-09-580-181-5
C 12	20	100.0	705	4	US-09-580-181-7
C 13	20	100.0	705	4	US-09-102-530-1
C 14	20	100.0	705	4	US-09-102-530-3
C 15	20	100.0	705	4	US-09-102-530-5
C 16	20	100.0	705	4	US-09-102-530-7
C 17	20	100.0	1557	1	US-08-385-229-3
C 18	20	100.0	1641	1	US-08-385-229-1
C 19	20	100.0	1641	2	US-08-650-000-1
C 20	20	100.0	1641	6	5395760-1
C 21	20	100.0	2224	4	US-08-477-347-2
C 22	20	100.0	2224	4	US-08-476-862-1
C 23	20	100.0	3683	4	US-09-844-634-3
C 24	19	95.0	34	1	US-08-050-319B-23
C 25	19	95.0	34	2	US-08-465-982-23
C 26	17	85.0	20	4	US-09-844-634-35
C 27	15.8	79.0	1712	2	US-08-632-598-1

C 28	15.8	79.0	1712	4	US-09-231-240-1	Sequence 1, Appli
C 29	14.8	74.0	2074	3	US-08-301-162-17	Sequence 17, Appl
C 30	14.8	74.0	2074	4	US-09-461-240-17	Sequence 17, Appl
C 31	14.8	74.0	2074	4	US-09-968-927-17	Sequence 17, Appl
C 32	14.4	72.0	1958	4	US-09-453-702B-113	Sequence 113, App
C 33	14.4	72.0	3321	4	US-08-486-270-1	Sequence 1, Appli
C 34	14.4	72.0	3321	3	US-08-367-264-1	Sequence 1, Appli
C 35	14.4	72.0	3321	4	US-09-153-757-1	Sequence 1, Appli
C 36	14.4	72.0	3330	1	US-08-072-574-1	Sequence 1, Appli
C 37	14.4	72.0	3382	4	US-08-538-526-2	Sequence 2, Appli
C 38	14.2	71.0	860	4	US-08-998-416-546	Sequence 546, App
C 39	14.2	71.0	1099	1	US-08-181-271A-25	Sequence 25, Appl
C 40	14.2	71.0	1099	1	US-08-449-315-25	Sequence 25, Appl
C 41	14.2	71.0	1099	1	US-08-444-803-25	Sequence 25, Appl
C 42	14.2	71.0	1099	1	US-08-449-043-25	Sequence 25, Appl
C 43	14.2	71.0	1099	1	US-08-456-265A-25	Sequence 25, Appl
C 44	14.2	71.0	1099	1	US-08-455-416-25	Sequence 25, Appl
C 45	14.2	71.0	1099	1	US-08-455-244-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
5395760-14/c
; Patent No. 5395760
; APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
; M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-A AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:14:
; LENGTH: 36
5395760-14

Query Match 100.0% Score 20; DB 6; Length 36;
Best Local Similarity 100.0% Pred. No. 0.062;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCAGCTCTGATGTTTCA 20
DB 21 ACACCAGCTCTGATGTTTCA 2

RESULT 2
US-08-266-080B-12/c
; Sequence 12, Application US/08266080B
; Patent No. 5606031
; GENERAL INFORMATION:
; APPLICANT: Jack Lille
; APPLICANT: Tadabiko Kohno
; APPLICANT: Duane Bonam
; APPLICANT: Mary S. Rosendahl
; TITLE OF INVENTION: Production of Biologically Active
; RECOMBINANT Neurotrophic Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-266-080B-12

Query Match 100.0%; Score 20; DB 1; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGTGATGTTTCA 20
|||||
DB 553 ACACCACGCTGTGATGTTTCA 534

RESULT 3
PCT-US95-05423-12/c
Sequence 12, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05423-12

Query Match 100.0%; Score 20; DB 5; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGTGATGTTTCA 20
|||||
DB 553 ACACCACGCTGTGATGTTTCA 534

RESULT 4
US-09-326-394-3/c
Sequence 3, Application US/09326394
Patent No. 6306820
GENERAL INFORMATION:
APPLICANT: Bendele, Allison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Edwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,394

;
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,587
; FILING DATE: 06-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,355
; FILING DATE: 23-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,315
; FILING DATE: 07-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/052,023
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zindrick, Thomas K.
; REGISTRATION NUMBER: 32,185
; REFERENCE/DOCKET NUMBER: A-430D
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-326-394-3

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
|||||
DB 415 ACACCACGCTGATGTTTCA 396

RESULT 5
US-09-580-235-1/c
; Sequence 1, Application US/09580235
; Patent No. 6433158
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/102,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 1:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-235-1

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
|||||
DB 415 ACACCACGCTGATGTTTCA 396

RESULT 6
US-09-580-235-3/c
; Sequence 3, Application US/09580235
; Patent No. 6433158
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/102,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-235-3

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
   |||||
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 7
US-09-580-235-5/c
; Sequence 5, Application US/09580235
; Patent No. 6433158
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/102,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; US-09-580-235-5

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
   |||||
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 8
US-09-580-235-7/c
; Sequence 7, Application US/09580235
; Patent No. 6433158
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,181
; FILING DATE: 26-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
   |||||
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 9
US-09-580-181-1/c
; Sequence 1, Application US/09580181
; Patent No. 6441136
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,181
; FILING DATE: 26-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; Mismatches 0; Indels 0; Gaps 0;
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; APPLICATION NUMBER: US 09/102,530
; FILING DATE: 22-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-181-1

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
|||||
DB 415 ACACCACGCTGATGTTTCA 396

RESULT 10
US-09-580-181-3/c
; Sequence 3, Application US/09580181
; Patent No. 6441136
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580.181
; FILING DATE: 26-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/102,530
; FILING DATE: 22-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-181-3

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
|||||
DB 415 ACACCACGCTGATGTTTCA 396

RESULT 11
US-09-580-181-5/c
; Sequence 5, Application US/09580181
; Patent No. 6441136
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580.181
; FILING DATE: 26-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/102,530
; FILING DATE: 22-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-181-5

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
|||||
DB 415 ACACCACGCTGATGTTTCA 396

RESULT 12

US-09-580-181-7/c
: Sequence 7, Application US/09580181
: Patent No. 6441136
: GENERAL INFORMATION:
: APPLICANT: Pettit, Dean
: TITLE OF INVENTION: Site Specific Protein Modification
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C Henry
: STREET: 51 University
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/580,181
: FILING DATE: 26-MAY-2000
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/102,530
: FILING DATE: 22-JUN-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2637
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..705
US-09-580-181-7

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGTGATGTTTCA 20
|||||
Db 415 ACACCACGCTGTGATGTTCA 396

RESULT 13

US-09-102-530-1/c
: Sequence 1, Application US/09102530
: Patent No. 6451986
: GENERAL INFORMATION:
: APPLICANT: Pettit, Dean
: TITLE OF INVENTION: Site Specific Protein Modification
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C Henry
: STREET: 51 University
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/102,530
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2637
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..705
US-09-102-530-1

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGTGATGTTTCA 20
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Db 415 ACACCACGCTGTGATGTTCA 396

RESULT 14

US-09-102-530-3/c
: Sequence 3, Application US/09102530
: Patent No. 6451986
: GENERAL INFORMATION:
: APPLICANT: Pettit, Dean
: TITLE OF INVENTION: Site Specific Protein Modification
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C Henry
: STREET: 51 University
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/102,530
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2637
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single

QY 1 ACACCACGCTCTGATGTTTCA 20
|||
Db 415 ACACCACGCTCTGATGTTTCA 396

GenCore version 5.1.3
Copyright (c) 1993-2002 Compugen Ltd.

OM nucleic - nucleic search, using sv model

Run on: December 5, 2002, 20:03:23 ; Search time 0.972171 Seconds
(without alignments)
8021.899 Million cell updates/sec

Title: us-09-856-937A-3

Perfect score: 20

Sequence: 1 aacacacgtctgatgtttca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 1	20	100.0	705	10	US-09-907-263-3
c 2	20	100.0	1641	10	US-09-758-124-1
c 3	20	100.0	2224	10	US-09-800-909-1
c 4	20	100.0	2224	10	US-09-800-908-2
c 5	20	100.0	3683	10	US-09-954-456-1187
c 6	15.8	79.0	306	10	US-09-974-300-3873
c 7	15.8	79.0	474	10	US-09-864-761-591
c 8	15.2	76.0	601	10	US-09-828-644-28
c 9	15.2	76.0	1659	10	US-09-740-288A-29
c 10	15.2	76.0	5617	10	US-09-917-800A-496
c 11	15.2	76.0	5921	12	US-10-040-919-1
c 12	15.2	76.0	6183	10	US-09-866-562-50
c 13	15.2	76.0	16428	10	US-09-764-847-1613
c 14	15.2	76.0	31834	10	US-09-764-847-1612
c 15	15.2	76.0	32035	10	US-09-764-847-1611
c 16	15.2	76.0	143306	10	US-09-729-920-3
c 17	14.8	74.0	237	10	US-09-783-590-8279
c 18	14.8	74.0	321	9	US-10-046-935-1825
c 19	14.8	74.0	321	9	US-09-878-178-1825

20	14.8	74.0	361	10	US-09-738-973-365	Sequence 365, Appl
21	14.8	74.0	456	10	US-09-960-352-1047	Sequence 1047, Ap
c 22	14.8	74.0	7215	10	US-09-070-927A-102	Sequence 102, App
23	14.8	74.0	7497	10	US-09-960-253-175	Sequence 175, App
24	14.8	74.0	7792	12	US-10-044-090-359	Sequence 359, App
c 25	14.8	74.0	48667	10	US-09-822-268A-3	Sequence 3, Appl
c 26	14.4	72.0	109	10	US-09-864-761-18345	Sequence 18345, A
c 27	14.4	72.0	387	10	US-09-864-761-1587	Sequence 1587, Ap
c 28	14.4	72.0	437	10	US-09-960-352-10610	Sequence 10610, A
c 29	14.2	71.0	372	10	US-09-770-791-329	Sequence 329, App
c 30	14.2	71.0	448	10	US-09-867-701-3249	Sequence 3249, Ap
c 31	14.2	71.0	467	10	US-09-867-701-2779	Sequence 2779, Ap
c 32	14.2	71.0	497	9	US-10-046-935-796	Sequence 796, App
c 33	14.2	71.0	497	9	US-09-878-178-796	Sequence 796, App
c 34	14.2	71.0	529	10	US-09-867-701-5479	Sequence 5479, Ap
c 35	14.2	71.0	537	10	US-09-070-927A-810	Sequence 810, App
c 36	14.2	71.0	553	9	US-10-046-935-1370	Sequence 1370, Ap
c 37	14.2	71.0	553	9	US-09-878-178-1370	Sequence 1370, Ap
c 38	14.2	71.0	595	10	US-09-777-564-619	Sequence 619, App
c 39	14.2	71.0	595	10	US-09-777-564-1452	Sequence 1452, Ap
c 40	14.2	71.0	723	10	US-09-878-574-4760	Sequence 4760, Ap
c 41	14.2	71.0	1224	10	US-09-730-525-21	Sequence 21, Appl
c 42	14.2	71.0	1224	10	US-09-730-917-21	Sequence 21, Appl
c 43	14.2	71.0	1455	10	US-09-815-242-6712	Sequence 6712, Ap
c 44	14.2	71.0	1658	9	US-10-002-344A-31	Sequence 31, Appl
c 45	14.2	71.0	1876	10	US-09-729-402-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

; Sequence 3, Application US/09907263

; Patent No. US20020119924A1

GENERAL INFORMATION:

APPLICANT: Bendele, Allison M.
Sennello, Regina M.

EDWARDS, Carl K.

TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
PROTEIN FOR TREATING TNF-MEDIATED DISEASES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Amgen Inc.

STREET: 1840 DeHavilland Drive

CITY: Thousand Oaks

STATE: CA

COUNTRY: US

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/907,263

FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/326,394

FILING DATE: 1999-06-04

APPLICATION NUMBER: US 60/036,355

FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/039,315

FILING DATE: 07-FEB-1997

APPLICATION NUMBER: US 60/052,023

FILING DATE: 09-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Zindrick, Thomas K.

REGISTRATION NUMBER: 32,185

REFERENCE/DOCKET NUMBER: A-430D

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

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; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-907-263-3

Query Match      100.0%; Score 20; DB 10; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
Db 415 ACACCACGCTCTGATGTTTCA 396

RESULT 2
US-09-758-124-1/c
; Sequence 1, Application US/09758124
; Patent No. US20020006391A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; APPLICANT: GOODWIN, Raymond G.
; APPLICANT: BECKMANN, M. Patricia
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
; FILE REFERENCE: A7895
; CURRENT APPLICATION NUMBER: US/09/758,124
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 08/953,268
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 08/555,629
; PRIOR FILING DATE: 1995-11-09
; PRIOR APPLICATION NUMBER: 08/468,453
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/038,765
; PRIOR FILING DATE: 1993-03-13
; PRIOR APPLICATION NUMBER: 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 1641
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1473)
; NAME/KEY: mat_peptide
; LOCATION: (154)..(1470)
; NAME/KEY: sig_peptide
; LOCATION: (88)..(153)
US-09-758-124-1

Query Match      100.0%; Score 20; DB 10; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
Db 568 ACACCACGCTCTGATGTTTCA 549

RESULT 3
US-09-800-909-1/c
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,862
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-09-800-909-1

Query Match      100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
Db 570 ACACCACGCTCTGATGTTTCA 551

RESULT 4
US-09-800-908-2/c
; Sequence 2, Application US/09800908
; Patent No. US2002011462A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
```

; BIGDA, Jacek
; BELETSKY, Igor
; METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,908
; FILING DATE: 08-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,347
; FILING DATE: <Unknown>
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-800-908-2

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTCGATGTTTCA 20
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Db 570 ACACCACGCTCGATGTTTCA 551

RESULT 5
US-09-954-456-1187/c
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1187
; LENGTH: 3683
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1187

Query Match 100.0%; Score 20; DB 10; Length 3683;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTCGATGTTTCA 20
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Db 570 ACACCACGCTCGATGTTTCA 551

RESULT 6
US-09-974-300-3873/c
; Sequence 3873, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3873
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-3873

Query Match 79.0%; Score 15.8; DB 10; Length 306;
Best Local Similarity 89.5%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CACCACGCTCGATGTTTCA 20
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Db 137 CACAACGCTTATGTTTCA 119

RESULT 7
US-09-864-761-591
; Sequence 591, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

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; Patent No. US20020015998A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20020015998A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00196US1
; CURRENT APPLICATION NUMBER: US/09/828,644
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,150
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,099
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,151
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,148
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,093
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,098
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/230,149
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-828-644-28

Query Match      76.0%;      Score 15.2; DB 10; Length 601;
Best Local Similarity 85.0%;      Pred No. 46;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACACGCTCTGATGTTTCA 20
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Db 573 ACACCAAGGTGATGTTCA 592

RESULT 9
US-09-740-288A-29
; Sequence 29, Application US/09740288A
; Patent No. US20010039042A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen
; APPLICANT: Kinney, Anthony
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Orozco, Emil
; TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
; FILE REFERENCE: BB1429 US NA
; CURRENT APPLICATION NUMBER: US/09/740,288A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/172929
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Glycine max
US-09-740-288A-29

Query Match      76.0%;      Score 15.2; DB 10; Length 1659;
Best Local Similarity 85.0%;      Pred. No. 55;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACACGCTCTGATGTTTCA 20
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Db 1069 ACAACAGGCTTATGTTTCA 1088

RESULT 10
US-09-917-800A-496/c
; Sequence 496, Application US/09917800A

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; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 496
; LENGTH: 5617
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AF052695
US-09-917-800A-496

Query Match 76.0%; Score 15.2; DB 10; Length 5617;
Best Local Similarity 85.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
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DB 1689 ACACCAGTCTCATGCTCTCA 1670

RESULT 11
US-10-040-919-1
; Sequence 1, Application US/10040919
; Patent No. US20020150563A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Michael
; APPLICANT: Lohmar, Patricia D.
; APPLICANT: Wood, Nancy L.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: GPI-122, A No. US20020150563A1e1 Glycophosphatidylinositol-Anchored Protein
; FILE REFERENCE: GI 5312A
; CURRENT APPLICATION NUMBER: US/10/040,919
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/277,837
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5921
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-919-1

Query Match 76.0%; Score 15.2; DB 12; Length 5921;
Best Local Similarity 85.0%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
||||| ||||| ||||| |||||
DB 3579 AACCCACGTCGATGTTTCA 3598

RESULT 12
US-09-866-562-50/c
; Sequence 50, Application US/09866562
; Patent No. US20020009758A1
; GENERAL INFORMATION:
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Klee, Jennifer
; APPLICANT: Switzer, Anne
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.502
; CURRENT APPLICATION NUMBER: US/09/866,562
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 50
; LENGTH: 6183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-562-50

Query Match 76.0%; Score 15.2; DB 10; Length 6183;
Best Local Similarity 85.0%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
||||| ||||| ||||| |||||
DB 4703 ACACCAAGTCTTATTTTCA 4684

RESULT 13
US-09-764-847-1613/c
; Sequence 1613, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1613
; LENGTH: 16428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1613

Query Match 76.0%; Score 15.2; DB 10; Length 16428;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
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DB 8425 ACACCTCGTCTCATATTTCA 8406

RESULT 14
US-09-764-847-1612/c
; Sequence 1612, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1612
; LENGTH: 31834
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1612

Query Match 76.0%; Score 15.2; DB 10; Length 31834;
Best Local Similarity 85.0%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACACCACGCTCTGATGTTTCA 20
||||| ||||| || |||||
Db 24037 ACACCTCGTCTCATATTTC 24018

RESULT 15
US-09-764-847-1611/c
; Sequence 1611, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1611
; LENGTH: 32035
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1611

Query Match 76.0%; Score 15.2; DB 10; Length 32035;
Best Local Similarity 85.0%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACACCACGCTCTGATGTTTCA 20
||||| ||||| || |||||
Db 24031 ACACCTCGTCTCATATTTC 24012

Search completed: December 6, 2002, 00:18:00
Job time : 21.9722 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:30:25 : Search time 41.4471 seconds
(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937A-4

Perfect score: 20
Sequence: 1 aggaactctgagcgtctttct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pi:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_on:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	480	9	AB030952	AB030952 Homo sapi
2	20	100.0	870	11	G15915	G15915 human STS C
3	20	100.0	1641	6	I36196	I36196 Sequence 1
4	20	100.0	2224	6	AR152033	AR152033 Sequence 1
5	20	100.0	2253	6	A78517	A78517 Sequence 1
6	20	100.0	2339	6	A26415	A26415 cDNA fragme
7	20	100.0	2394	9	HUMTNFRII	M55994 Human tumor
8	20	100.0	2613	9	HSTNFR2S10	U52165 Human tumor
9	20	100.0	3380	11	G26865	G26865 human STS S
10	20	100.0	3492	9	S63368	S63368 Homo sapien
11	20	100.0	3683	6	AX333705	AX333705 Sequence
12	20	100.0	3683	6	AX348016	AX348016 Sequence
13	20	100.0	3683	6	AX348018	AX348018 Sequence
14	20	100.0	3683	6	AX348020	AX348020 Sequence
15	20	100.0	3683	9	HUMNFR	M32315 Human tumor
16	20	100.0	115602	9	HS1118D24	AL031276 Human DNA
17	20	100.0	122105	2	AL355998	AL355998 Homo sapi
18	20	100.0	187877	2	AC023251	AC023251 Homo sapi
19	19	95.0	25	6	AX348010	AX348010 Sequence
20	19	95.0	166555	2	AC009197	AC009197 Rattus no
21	19	95.0	188314	9	AC009494	AC009494 Homo sapi
22	19	95.0	230334	10	AC112521	AC112521 Mus muscu
23	18.4	92.0	104630	9	AC007397	AC007397 Homo sapi
24	18.4	92.0	108778	9	AC005194	AC005194 Homo sapi
25	18.4	92.0	110348	2	AC098539	AC098539 Rattus no
26	18.4	92.0	139398	9	AC025836	AC025836 Homo sapi
27	18.4	92.0	153360	2	AC129073	AC129073 Felis cat
28	18.4	92.0	154485	2	AC068934	AC068934 Homo sapi
29	18.4	92.0	157976	2	AC127476	AC127476 Felis cat
30	18.4	92.0	161339	9	AC007535	AC007535 Homo sapi
31	18.4	92.0	165889	10	AL606841	AL606841 Mouse DNA
32	18.4	92.0	169898	2	AC016585	AC016585 Homo sapi
33	18.4	92.0	171529	2	AC023021	AC023021 Homo sapi
34	18.4	92.0	172574	2	AC011121	AC011121 Homo sapi
35	18.4	92.0	182823	9	AC016638	AC016638 Homo sapi
36	18.4	92.0	197065	9	AC090686	AC090686 Homo sapi
37	18.4	92.0	202249	2	AC095427	AC095427 Rattus no
38	18.4	92.0	204493	2	AC111047	AC111047 Mus muscu
39	18.4	92.0	208709	2	AL592162	AL592162 Mus muscu
40	18.4	92.0	217807	2	AC079469	AC079469 Homo sapi
41	18	90.0	65792	2	AC117664	AC117664 Mus muscu
42	18	90.0	164331	9	AC016254	AC016254 Homo sapi
43	17.4	87.0	1716	5	DRAJ3200	AJ003200 Danio rer
44	17.4	87.0	1813	5	AF168008	AF168008 Danio rer
45	17.4	87.0	40036	2	AC101084	AC101084 Mus muscu

ALIGNMENTS

RESULT 1
AB030952
LOCUS

DEFINITION

AB030952 Homo sapiens TNFR2 gene for tumor necrosis factor receptor 2, partial cds.

ACCESSION AB030952.1 GI:6683135

VERSION tumor necrosis factor receptor 2; TNFR2.

KEYWORDS Homo sapiens DNA.

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AB030952 Tsuchiya,N., Komata,T., Matsushita,M., Ohashi,J. and Tokunaga,K.
TITLE New single nucleotide polymorphisms in the coding region of human

JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 480)
AUTHORS Komata,T., Tsuchiya,N. and Tokunaga,K.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1999) Tae Komata, University of Tokyo, Department of Human Genetics, Graduate School of Medicine, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:tae@m.u-tokyo.ac.jp, Tel:81-3-5841-3693, Fax:81-3-5802-8619)

FEATURES
source 1. .480
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
78. .>480
/number=10
78. .358
/gene="TNFR2"
CDS <78. .358
/gene="TNFR2"
/codon_start=3
/product="tumor necrosis factor receptor 2"
/protein_id="BAA89055.1"
/db_xref="GI:6683136"
/translation="SSPGHGHTQVNVTCIVNWCSSSDHSSQCSQASSTMGDTSSPS
ESPKDEQVPFSSKECAFRSQLETPETLLGSTEEKPLPLGVDPAGMKPS"
variation 381

BASE COUNT 93 a 159 c 137 g 91 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 454 AGGACTCTGAGGCTCTTTCT 473

RESULT 2
GI5915
LOCUS human STS CHLC.UTR_02819_M32315.P65016 clone UTR_02819_M32315,
DEFINITION 870 bp DNA linear STS 19-JAN-1996
sequence tagged site.
GI5915
GI5915.1 GI:1161804
VERSION STS; STS sequence; primer; sequence tagged site.
KEYWORDS Homo sapiens vector-pJCP1 host=E.coli dut+ung+ (DH10B) Marker
SOURCE Selected genomic DNA prepared from XY individual of French nationality.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: UTR_02819_M32315, CHLC.UTR_02819_M32315.T36190
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu

Primer A: CCCTGACTCTCTGTGACCTG
Primer B: GTCCTCATGGGTGACTCAGG
STS size: 206
PCR Profile: denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C

extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C
Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 ul

Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3

Prepared with primer pairs derived from M32315.
FEATURES
source 1. .870
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
STS 272. .477
primer_bind 272. .291
primer_bind complement(458. .477)
BASE COUNT 157 a 246 c 279 g 188 t
ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 870;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGACTCTGAGGCTCTTTCT 20
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Db 96 AGGACTCTGAGGCTCTTTCT 115

RESULT 3
I36196
LOCUS I36196 1641 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5605690.
ACCESSION I36196
VERSION I36196.1 GI:2086709
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1641)
AUTHORS Jacobs,C.A. and Smith,C.A.
TITLE Methods of lowering active TNF-.alpha. levels in mammals using tumor necrosis factor receptor
JOURNAL Patent: US 5605690-A 1 25-FEB-1997;
FEATURES Location/Qualifiers
source 1. .1641
BASE COUNT 328 a 544 c 502 g 267 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1641;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGACTCTGAGGCTCTTTCT 20
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Db 1569 AGGACTCTGAGGCTCTTTCT 1588

RESULT 4
AR152033
LOCUS AR152033 2224 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6232446.
ACCESSION AR152033
VERSION AR152033.1 GI:15118083
KEYWORDS

SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 2224)
AUTHORS
Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
TITLE
TNF ligands
JOURNAL
Patent: US 6232446-A 2 15-MAY-2001;
FEATURES
Location/Qualifiers
1..2224
/organism="unknown"
BASE COUNT
435 a 698 c 689 g 402 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 2224;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590
RESULT 5
A78517
LOCUS
A78517 2253 bp DNA linear PAT 19-OCT-1999
DEFINITION
Sequence 1 from Patent EP0585939.
ACCESSION
A78517
VERSION
A78517.1 GI:6090179
KEYWORDS
unidentified.
SOURCE
unidentified.
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 2253)
AUTHORS
Mett,I. and Wallach,D.
TITLE
TNF LIGANDS
JOURNAL
Patent: EP 0585939-A 1 09-MAR-1994;
YEDA RES & DEV (IL)
FEATURES
Location/Qualifiers
1..2253
/organism="unidentified"
/db_xref="taxon:32644"
90..1475
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB58915.1"
/db_xref="GI:6090180"
/translation="NAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLRE
YVDTAQMCCKSPGOHAKVFCTXTSDTDCDCEDSTYTQLWNWVPECLSGCRSS
DYVQACTREQNRICRPHQICNSVAIPGNAEGSTGDFALPVGTVGALGLLIIGVNCVIMTQV
CRPCAPGTFSTNTSDICRPHQICNSVAIPGNAEGSTGDFALPVGTVGALGLLIIGVNCVIMTQV
PVSTRSQHTPEPSTAPSTFLPMGPSPPAEGSTGDFALPVGTVGALGLLIIGVNCVIMTQV
GVVNCVIMTQVKKKLCLOREAKVPHLPADKARGTQGPQOHLITAPSSSSSSLESS
ASALDRAPTRNOPAPGVEASGAGEARASTGSSDSPGGHGTQVNTVCIVNVCSSD
HSSCCSSOASSMTGDTDSPSPKDEQVPFSKECAFRSQLETPETLLGSTEKPLP
LGVPDAGMKPS"
BASE COUNT
440 a 709 c 698 g 406 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 2253;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590
RESULT 6
A26415
LOCUS
A26415 2339 bp DNA linear PAT 26-APR-1995
DEFINITION
cDNA fragment for (75kd TNF-BP) tumor necrosis factor binding
protein from patent EP0417563.
ACCESSION
A26415

VERSION
KEYWORDS
A26415.1 GI:904970
synthetic construct.
SOURCE
synthetic sequences
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 2339)
AUTHORS
Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
Schlaeger,E.J.
TITLE
TNF-binding proteins
JOURNAL
Patent: EP 0417563-A 27 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
FEATURES
Location/Qualifiers
1..2339
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..1179
/codon_start=1
/translation_table=11
/product="75kd TNF-BP"
/protein_id="CAA01806.1"
/db_xref="GI:904971"
/translation="SDSVCDSCEDSTYTQLWNWVPECLSGCRSSDQVETQACTRQ
NRICTRPGWYCALSKQEGRLCAPLKRPGVGARPGTETSDVVKCPAGPTFSNT
TSSYDIDCRPHQICNSVAIPGNAEGSTGDFALPVGTVGALGLLIIGVNCVIMTQV
PEPTAPSTFLPMGPSPPAEGSTGDFALPVGTVGALGLLIIGVNCVIMTQV
KKPLCLQREAKVPHLPADKARGTQGPQOHLITAPSSSSSSLESSASALDRAPTRN
QPOAPGVEASGAGEARASTGSSDSPGGHGTQVNTVCIVNVCSSDSSHSSQCSOASS
TMGDTDSPSPKDEQVPFSKECAFRSQLETPETLLGSTEKPLPGLGVPDAGMKPS"
BASE COUNT
494 a 720 c 685 g 440 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 2339;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1274 AGGACTCTGAGGCTCTTTCT 1293
RESULT 7
HUMTNFR11
LOCUS
HUMTNFR11 2394 bp mRNA linear PRI 03-SEP-1994
DEFINITION
Human tumor necrosis factor receptor II (TNFR11) mRNA, complete
cds.
ACCESSION
M55994 M38549
VERSION
M55994.1 GI:339757
KEYWORDS
glycoprotein; nerve growth factor receptor related; transmembrane
protein; tumor necrosis factor receptor; tumor necrosis factor
receptor II.
SOURCE
Human histiocytic lymphoma cell line U937, cDNA to mRNA.
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
Kohn,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W.,
Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
TITLE
A second tumor necrosis factor receptor gene product can shed a
naturally occurring tumor necrosis factor inhibitor
Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)
JOURNAL
MEDLINE
91045991
PUBMED
2172983
FEATURES
Location/Qualifiers
1..2394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/cell_type="histiocytic lymphoma"
1..2394
/gene="TNFR11"
93..1478
/gene="TNFR11"

/note="603. .611 and 669. .677 glycosylation site: 861. .947
transmembrane domain: 948. .1478 cytoplasmic domain;
159,860 extracellular domain"
/codon_start=1
/evidence=experimental
/product="tumor necrosis factor receptor"
/protein_id="AAA36755.1"
/db_xref="GI:339758"
/translation="MAPVAVMAALAVGLELWAAHAALPAQVAFTPYAPPGSTCRLRE
YDDTAOMCCSKSPGQHAQVCTKTSDTVCDSCEDSTYTQLMNWPCLSCGRCS
DQVETQACTREONRICTRPGWYCALSKQEGCLCAPLKRCPGFGVARPGTSDVQ
CKPCAPGTSNTSTDICRPHQICNVVAIPGNASMDAVCTSTPTSRMAPGAVHLPO
PVSTRQHTQPTPEPSTAPSTFLLPMGSPPAEGSTGDFALPGLIVGVATGLLII
GVNVCYMTQVKKKPLCLQREAKVPHLPADKARGTQGPQEOHLLITAPSSVSSSLESS
ASALDRAPTRNQAPQPGVEASGAGEARASTGSSDSPGGHGTQVNTCIVNVCSSSD
HSQCSSASSTMGTDSPSEPKDEQVFPFKNECATRSQLETPTLLGSTEARPLP
LGVPDAGMKPS"
93. .158
/gene="TNFR1"
/note="putative"
159. .1475
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/product="tumor necrosis factor receptor"
/note="putative"
BASE COUNT 484 a 743 c 739 g 428 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 2394;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGACTCTGAGGCTCTTCT 20
|||||
Db 1574 AGGACTCTGAGGCTCTTCT 1593
RESULT 8
HSTNFR2S10 2613 bp DNA linear PRI 31-JUL-1996
LOCUS Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 10 and
DEFINITION complete cds.
VERSION U52165.1 GI:1469539
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2613)
Beltzinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
Lepaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and
Brodeur,G.M.
TITLE Physical mapping and genomic structure of the human TNFR2 gene
JOURNAL Genomics 35 (1), 94-100 (1996)
MEDLINE 96299745
PUBMED 8661109
REFERENCE 2 (bases 1 to 2613)
Beltzinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
Lepaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and
Brodeur,G.M.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1996) Christian P. Beltzinger, Division of
Oncology, ARC Rm. 902 D, Children's Hospital of Philadelphia, 324
South 34th Street, Philadelphia, PA 19104-4318, USA
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DEFINITION
ACCESSION G26865
VERSION G26865.1 GI:1375115
KEYWORDS STS: STS sequence; primer: sequence tagged site.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3380)
Myers,R.M.
REFERENCE 1
AUTHORS
JOURNAL
COMMENT Unpublished (1995)
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CCCACCACCTAGGACTCTGA
Primer B: CACAGAGAGTCAGGACTTGC
STS size: 201
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR cycles: 30

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U52160.1:1. .106,U52161.1:1. .336,U52162.1:1. .218,
U52163.1:1. .58,U52164.1:1. .234,1. .2613)
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/number=9
125. .2613
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/number=10
BASE COUNT 553 a 750 c 742 g 568 t
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Query Match 100.0%; Score 20; DB 9; Length 2613;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGACTCTGAGGCTCTTCT 20
|||||
Db 501 AGGACTCTGAGGCTCTTCT 520
RESULT 9
G26865
LOCUS human STS SHGC-31494, sequence tagged site.
DEFINITION
ACCESSION G26865
VERSION G26865.1 GI:1375115
KEYWORDS STS: STS sequence; primer: sequence tagged site.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3380)
Myers,R.M.
REFERENCE 1
AUTHORS
JOURNAL
COMMENT Unpublished (1995)
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CCCACCACCTAGGACTCTGA
Primer B: CACAGAGAGTCAGGACTTGC
STS size: 201
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
each 1 uM
Primer: each 200 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from M32315
-- Washington University/Merck EST sequence.

FEATURES
source

Location/Qualifiers
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Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 10

S63368

LOCUS S63368 3492 bp mRNA linear PRI 06-MAR-2001
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, partial cds.
ACCESSION S63368

VERSION S63368.1 GI:235648

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3492)

Dembic, Z., Loetscher, H., Gubler, U., Pan, Y. C., Lahm, H. W., Gentz, R.,

Brockhaus, M. and Lesslauer, W.

Two human TNF receptors have similar extracellular, but distinct

intracellular, domain sequences

Cytokine 2 (4), 231-237 (1990)

JOURNAL

MEDLINE

PUBMED

1966549

GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 63368] from the original journal article.

This sequence comes from Figure 1.

Location/Qualifiers

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RESULT 11

AX333705

LOCUS AX333705 3683 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 4214 from Patent WO0194629.

ACCESSION AX333705

VERSION AX333705.1 GI:18124424

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D. R. and Weaver, Z.,

Cancer gene determination and therapeutic screening using signature

gene sets

Patent: WO 0194629-A 4214 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers

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RESULT 12

AX348016

LOCUS AX348016 3683 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 49 from Patent EP1172444.

ACCESSION AX348016

VERSION AX348016.1 GI:18614126

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Schreiber, S., Hampe, J. and Mascheretti, S.

Diagnostic use of polymorphisms in the gene coding for the tnfr

receptor II and method for detecting non-responders to anti-tnf

therapy

Patent: EP 1172444-A 49 16-JAN-2002;

Conaris Research Institute GmbH (DE)

Location/Qualifiers

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Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 13
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LOCUS
DEFINITION Sequence 51 from Patent EP1172444.
ACCESSION AX348018
VERSION AX348018.1 GI:18614128
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Schreiber,S., Hampe,J. and Mascheretti,S.
TITLE Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
JOURNAL Patent: EP 1172444-A 51 16-JAN-2002;
Conaris Research Institute GmbH (DE)
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LOCUS
DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION M32315
VERSION M32315.1 GI:189185
KEYWORDS c-myc proto-oncogene; necrosis factor receptor.
SOURCE Homo sapiens lung CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3683)
AUTHORS Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P.,
Jerzy,R., Dower,S.K., Cosman,D. and Goodwin,R.G.
TITLE A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins
JOURNAL Science 248 (4958), 1019-1023 (1990)
MEDLINE 90260639
PUBMED 2160731
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by C.A.Smith, 30-MAR-1990, for release after publication.
FEATURES
Location/Qualifiers
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ACCESSION AX348020
VERSION AX348020.1 GI:18614130
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Schreiber,S., Hampe,J. and Mascheretti,S.
TITLE Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
JOURNAL Patent: EP 1172444-A 53 16-JAN-2002;
Conaris Research Institute GmbH (DE)
FEATURES
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mat_peptide 780 a 1098 c 1088 g 717 t
BASE COUNT 780 a 1098 c 1088 g 717 t
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION M32315
VERSION M32315.1 GI:189185
KEYWORDS c-myc proto-oncogene; necrosis factor receptor.
SOURCE Homo sapiens lung CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3683)
AUTHORS Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P.,
Jerzy,R., Dower,S.K., Cosman,D. and Goodwin,R.G.
TITLE A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins
JOURNAL Science 248 (4958), 1019-1023 (1990)
MEDLINE 90260639
PUBMED 2160731
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by C.A.Smith, 30-MAR-1990, for release after publication.
FEATURES
Location/Qualifiers
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 4.80891 Seconds
(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937A-4

Perfect score: 20

Sequence: 1 aggaactctgaggtcttctt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	1641	AAQ49931	TNF-R cDNA. Homo
5	20	100.0	1641	AAQ45224	Sequence encoding
6	20	100.0	2339	AAQ10956	Encodes human 75kD
7	20	100.0	2339	AAQ209171	Human tumour necro
8	20	100.0	2339	AAH48860	Human TNFRP-associ
9	20	100.0	2393	AAQ10907	40kD TNF inhibitor

10	20	100.0	2394	22	AAC83951	Human 40 kDa TNF 1
11	20	100.0	2613	21	AAA49207	Human tumour necro
12	20	100.0	3683	24	ABK83997	Human cDNA differe
13	20	100.0	3683	24	ABL65877	Lung cancer relate
14	20	100.0	3683	24	ABK33465	Human TNF receptor
15	20	100.0	3683	24	ABK33466	Human TNF receptor
16	20	100.0	3683	24	ABK33467	Human TNF receptor
17	19	95.0	25	24	ABK33459	Human TNF-receptor
18	18.4	92.0	2224	16	AAQ89544	p75 Tumour Necrosi
19	17	85.0	485	21	AAQ03830	Human secreted pro
20	17	85.0	1280	17	AAT33354	Human Ich-2 protei
C 21	16.8	84.0	322	23	ABV06635	Human prostate exp
C 22	16.8	84.0	407	23	ABV36584	Human prostate exp
C 23	16.8	84.0	480	22	ABA52150	Human prostate exp
C 24	16.8	84.0	480	22	ABA21957	Human foetal liver
C 25	16.8	84.0	480	22	AAK00430	Probe #423 for gen
C 26	16.8	84.0	480	22	AAK25873	Human brain expres
C 27	16.8	84.0	480	22	AAI10503	Human bone marrow
C 28	16.8	84.0	480	22	AAI31757	Probe #436 for gen
C 29	16.8	84.0	480	22	AAI00436	Probe #443 used to
C 30	16.8	84.0	480	22	ABS00456	Probe #427 used to
C 31	16.8	84.0	580	24	ABL83157	Human genome-deriv
C 32	16.8	84.0	966	22	ABA64903	Human ovarian canc
C 33	16.8	84.0	966	22	ABA64784	Human breast cell
C 34	16.8	84.0	966	22	ABA31902	Human foetal liver
C 35	16.8	84.0	966	22	ABA13216	Probe #10368 for g
C 36	16.8	84.0	966	22	AAK38947	Human brain expres
C 37	16.8	84.0	966	22	AAI19757	Human bone marrow
C 38	16.8	84.0	966	22	AAI44953	Probe #9690 for ge
C 39	16.8	84.0	966	22	AAI05474	Probe #13639 used
C 40	16.8	84.0	966	24	ABS13031	Probe #5465 used t
C 41	16.8	84.0	1086	22	ABA46796	Human genome-deriv
C 42	16.8	84.0	1086	22	ABA47311	Human breast cell
C 43	16.8	84.0	1086	22	ABA64676	Human foetal liver
C 44	16.8	84.0	1086	22	ABA65196	Human foetal liver
C 45	16.8	84.0	1086	22	ABA31800	Probe #10266 for g

ALIGNMENTS

RESULT 1
AAA49210
ID AAA49210 standard; DNA; 20 BP.
XX
AC AAA49210;
XX
DT 22-NOV-2000 (first entry)
XX
XX Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-7.

DE Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-7.
XX
KW Human: tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
XX osteoporosis; PCR primer; ss.
OS Homo sapiens.

XX
XX WO2000032826-A1.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US28403.
XX
PR 30-NOV-1998; 98US-0110268.
XX
XX (UYDR-) UNIV DREXEL.
XX
XX Spotilla LD;
XX
XX WPI; 2000-412362/35.

XX
XX Identifying individuals at risk of developing osteoporosis comprises
PT assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
PT in a DNA sample from an individual -

XX Example 3; Page 12; 21pp; English.

XX The present sequence is a PCR primer for the three polymorphic sites

CC within exon 10 of the human tumour necrosis factor alpha receptor 2

CC (THFR2) gene. By determining the genotype of an individual it is possible

CC to identify those at risk of osteoporosis, which is characterised by low

CC bone density and fragile bones, later in life. Those at greatest risk are

CC those who possess allele 1, which is the rarest allele. This is

CC particularly useful as many cases of osteoporosis go undetected at

CC present. The primer can be used to determine an individual's genotype,

CC and, therefore, their risk of osteoporosis.

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 other;

SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20

Db 1 AGGACTCTGAGGCTCTTTCT 20

RESULT 2

AA12093

ID AAX12093 standard; DNA; 201 BP.

XX AC AAX12093;

XX DT 30-MAR-1999 (first entry)

XX DE Human biallelic polymorphic DNA fragment M32315b.

XX KW Polymorphism: biallelic; human; forensic; paternity testing; disease;

XX KW detection; phenotypic typing; characteristic; infection; hereditary;

XX KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;

XX KW treatment; marker; ss.

XX OS Homo sapiens.

XX IN WO9820165-A2.

XX PD 14-MAY-1998.

XX PF 05-NOV-1997; 97WO-US20313.

XX PR 06-NOV-1996; 96US-0030455.

XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX P1 Hudson T, Lander ES, Wang D;

XX WP1; 1998-286974/25.

XX New isolated nucleic acid segments from the human genome - used for

PT determining polymorphic forms for use in e.g. forensics, paternity

PT testing or phenotypic typing for disease

XX Claim 1; Page 219; 310pp; English.

XX AAX10269-X12937 are human DNA fragments which contain biallelic

CC polymorphic markers which have been isolated using the primers

CC represented in AAX09121-X10268. The base occupying the polymorphic site

CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments

CC can be used in methods for determining polymorphic forms in an individual

CC for use in e.g. forensics, paternity testing or for phenotypic typing for

CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan

CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,

CC familial hypercholesterolemia, polycystic kidney disease, hereditary

CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary

CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos

CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,

CC autoimmune diseases, inflammation, cancer, diseases of the nervous

CC system, infection by pathogenic microorganisms, and characteristics such

CC as longevity, appearance (e.g. baldness, obesity), strength, speed,

CC endurance, fertility, and susceptibility or receptivity to particular

CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid

CC segments can also be used to produce medicaments for the treatment or

CC prophylaxis of such diseases.

XX Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

SQ Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

Query Match 100.0%; Score 20; DB 19; Length 201;

Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20

Db 11 AGGACTCTGAGGCTCTTTCT 30

RESULT 3

AAQ10990

ID AAQ10990 standard; cDNA to mRNA; 1640 BP.

XX AC AAQ10990;

XX DT 24-MAY-1991 (first entry)

XX DE Partial sequence of hTNF-R clone 1.

XX KW Tumour necrosis factor receptor; immune response; inflammation;

XX KW cachexia; septic shock; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 88..1473

FT mat_peptide 154..1470

FT sig_peptide 88..153

FT EP418014-A.

XX PN 20-MAR-1991.

XX PF 10-SEP-1990; 90EP-0309875.

XX PR 10-MAY-1990; 90US-0523635.

XX PR 11-SEP-1989; 89US-0405370.

XX PR 13-OCT-1989; 89US-0421417.

XX PA (IMMU-) IMMUNEX CORP.

XX PI Smith CA, Goodwin RG, Beckmann PM;

XX WP1; 1991-082230/12.

XX P-PSDB; AAR11141.

XX New tumour necrosis factor -alpha and -beta receptors - and DNA

PT encoding these used to regulate immune responses in treatment of

PT cachexia, septic shock or side-effects of cytokine therapy.

XX Claim 1; Fig 2; 41pp; English.

XX The sequence was obt'd. from a clone isolated from library prep'd.

CC from a human fibroblast cell line, WI-26 VA4 (ATCC CCL 95.1).

CC The clone is deposited as Accession No. 68088 under the name

CC PCAV/NOT-TNF-R. The DNA can be truncated to produce sequences which

CC express soluble receptor comprising residues 1-235, 1-185 or 1-163

CC of the protein.

CC See also AAQ10991.

SQ Sequence 1640 BP; 328 A; 543 C; 502 G; 267 T; 0 other:

Query Match 100.0%; Score 20; DB 12; Length 1640;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGGCTCTTCT 20
 ||||||||||||||||
 DB 1569 AGGACTCTGAGGCTCTTCT 1588

RESULT 4
 AAQ49931
 ID AAQ49931 standard; cDNA to mRNA; 1641 BP.

AC AAQ49931;
 DT 29-APR-1994 (first entry)
 DE TNF-R CDNA.

Human: tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
 IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
 rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
 pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
 graft versus host disease; sepsis; inflammation; allergy;
 autoimmune dysfunction; ss.

OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 88..1473
 FT /*tag= a
 FT /product= hTNF-R
 FT sig_peptide 88..153
 FT /*tag= b
 FT mat_peptide 154..1470
 FT /*tag= c

XX
 XX
 PN W09319777-A.
 XX
 PD 14-OCT-1993.
 XX
 XX
 PF 26-MAR-1993; 93WO-US02938.
 XX
 PR 30-MAR-1992; 92US-0860710.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Smith CA;
 XX
 DR WPI: 1993-336592/42.
 DR P-PSDB; AAR42058.

XX
 XX
 PT New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
 XX
 PS Disclosure; Fig 2; 85pp; English.

XX
 CC The sequences given in AAQ49931-32 encode human tumour necrosis factor
 CC receptor (TNF-R) and the sequences in AAQ49931-34 encode human
 CC interleukin-1 receptor (IL-1R). These sequences were used in the
 CC production of a fusion protein which conformed to one of the
 CC formulae:
 CC TNF-R-linker-TNF-R-linker-IL-1R
 CC IL-1R-linker-TNF-R-linker-TNF-R or
 CC TNF-R-linker-TNF-R
 CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
 CC Ser, Thr and Ala. These linkers separate the individual moieties
 CC by such a distance that each component of the fusion protein is
 CC capable of folding into the secondary or tertiary structure required
 CC for its biological activity. These fusion proteins may be used in

CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 CC particularly in conditions in which both TNF and IL-1 play a causative
 CC role. They may be used to treat cachexia, rheumatoid arthritis,
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
 CC cerebral malaria, allograft and xenograft rejection in graft versus
 CC host disease, sepsis, septic shock, inflammation, allergies and
 CC autoimmune dysfunctions.

SQ Sequence 1641 BP; 328 A; 544 C; 502 G; 267 T; 0 other:

Query Match 100.0%; Score 20; DB 14; Length 1641;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGGCTCTTCT 20
 ||||||||||||||||
 DB 1569 AGGACTCTGAGGCTCTTCT 1588

RESULT 5
 AAQ45224
 ID AAQ45224 standard; cDNA; 1641 BP.

AC AAQ45224;
 DT 07-OCT-1994 (first entry)
 DE Sequence encoding human tumour necrosis factor receptor type I
 DE (TNFRI).
 XX
 XX
 DE Tumour necrosis factor receptor; type I; TNFRI; arthritis therapy; ss.
 XX
 XX
 KM Homo sapiens.
 XX
 OS
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 154..1470
 FT /*tag= a
 FT sig_peptide 88..153
 FT /*tag= b

XX
 XX
 PN W09406476-A.
 XX
 PD 31-MAR-1994.
 XX
 XX
 PF 14-SEP-1993; 93WO-US08666.
 XX
 PR 15-SEP-1992; 92US-0946236.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Jacobs CA, Smith CA;
 XX
 DR WPI: 1994-118172/14.
 DR P-PSDB; AAR51002.

XX
 XX
 PT Treating TNF mediated inflammatory diseases with TNF antagonist -
 PT esp. soluble form of TNF receptor, opt. as fusion protein with
 PT human immunoglobulin Fc region, esp. for treating arthritis
 XX
 PS Disclosure; Page 28-30; 47pp; English.

XX
 CC AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
 CC cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein
 CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
 CC TNFRI was described in Smith et al., Science 248:1019, 1990. Clone 1
 CC is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The
 CC preferred TNFRs of the present invention are soluble forms of TNFRI
 CC and TNFRII having at least 20 AAs. Soluble TNFR constructs are
 CC devoid of a transmembrane region but retain the ability to bind TNF.
 CC Examples of soluble TNFRs are hTNFRIdelta235, hTNFRIdelta185 and
 CC hTNFRIdelta163 which encode respectively AAs 1-235, 1-185 and 1-163
 CC of AAR51002. An equivalent soluble TNFR is hTNFRIdeltaX wherein X
 CC is selected from any one of AAs 163-235 of AAR51002.


```

RESULT 8
AAH48860
ID AAH48860 standard; DNA: 2339 BP.
XX
AC AAH48860;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human TNFBP-associated DNA #2.
XX
KW TNF: tumor necrosis factor binding protein; TNFBP; treatment:
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotocozal; treatment; meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..1179
FT CDS /*tag= a
FT /product= "TNFBP-associated protein"
XX
PN EP1132471-A2.
XX
PD 12-SEP-2001.
XX
PV 31-AUG-1990; 2001EP-0108117.
XX
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
PR 20-APR-1990; 90CH-0001347.
PR 31-AUG-1990; 90EP-0116707.
PR 31-AUG-1990; 99EP-0100703.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlegel E;
XX
DR WPI: 2001-559312/63.
DR P-PSDB: AAB86818.
XX
PT New homogeneous, insoluble proteins that bind tumor necrosis factor
PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
XX
PS Claim 4a; Fig 4; 26pp; German.
XX
CC This invention describes novel insoluble proteins (I), also their
CC (insoluble) fragments and pharmaceutically acceptable salts, able to bind
CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC invention have antiinflammatory, immunosuppressive, antibacterial,
CC antiprotocozal activity. (I), and related recombinant proteins, are used
CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC sepsis; development of autoimmune glomerulonephritis and cerebral
CC malaria. Also (I), or antibodies specific for them, are used for
CC diagnostic determination of TNF in body fluids; for affinity purification
CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC human TNF binding protein described in the method of the invention.
XX
SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 22; Length 2339;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGACTCTGAGGCTCTTCT 20
DB 1274 AGGACTCTGAGGCTCTTCT 1293

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ID AAQ10907 standard; cDNA; 2393 BP.
XX
AC AAQ10907;
XX
DT 13-MAY-1991 (first entry)
XX
DE 40kd TNF inhibitor precursor gene in c40DK#6.
XX
KW Tumour necrosis factor; inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 93..1478
FT CDS /*tag= a
XX
PN AU9058976-A.
XX
PD 24-JAN-1991.
XX
PV 16-JUL-1990; 90AU-0058976.
XX
PR 07-FEB-1990; 90US-0479661.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
XX
PA (SYNE-) SYNERGEN INC.
XX
DR WPI: 1991-073847/11.
DR P-PSDB: AAR11001.
XX
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
XX
PS Disclosure; Fig 39; 142pp; English.
XX
CC The sequence encodes the entire 40 kD TNF inhibitor. The clone from
CC which the sequence was obt'd. was isolated from a cDNA library
CC prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
CC gene can be inserted into expression vectors for prep'n. of TNF
CC inhibitor for use in the treatment of inflammatory and degenerative
CC diseases.
XX
SQ See also AAQ10878, AAQ10884 and AAQ10883.
XX
SQ Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 12; Length 2393;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGACTCTGAGGCTCTTCT 20
DB 1573 AGGACTCTGAGGCTCTTCT 1592

```

```

RESULT 10
AAC83951
ID AAC83951 standard; DNA: 2394 BP.
XX
AC AAC83951;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 40 kDa TNF inhibitor precursor coding sequence.
XX
KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human; lymphotoxin; ss.
XX
OS Homo sapiens.
XX
PN US6143866-A.
XX
PD 07-NOV-2000.

```

[illegible]

FT	allele	replace (593,G), (598,T), (620,T)
FT		/tag= e
FT	allele	/label= allele_4
FT	allele	replace (593,A), (598,T), (620,C)
FT		/tag= f
FT		/label= allele_5
PN		
XX	WO200032826-A1.	
XX		
PD	08-JUN-2000.	
XX		
PF	30-NOV-1999;	99WO-US28403.
XX		
PR	30-NOV-1998;	98US-0110268.
XX		
PA	(UYDR-) UNIV DREXEL.	
XX		
PI	Spot11a LD;	
XX		
DR	WPI: 2000-412362/35.	
XX		
PT	Identifying individuals at risk of developing osteoporosis comprises	
PT	assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene	
PT	in a DNA sample from an individual -	
XX		
PS	Claim 2: Page 17-18; 21pp; English.	
XX		
CC	The present sequence comprises exon 10 of the human tumour necrosis	
CC	factor alpha receptor 2 (TFR2) gene. The sequence contains three	
CC	polymorphic sites. By determining the genotype of an individual it is	
CC	possible to identify those at risk of osteoporosis, which is	
CC	characterised by low bone density and fragile bones, later in life. Those	
CC	at greatest risk are those who possess allele 1, which is the rarest	
CC	allele. This is particularly useful as many cases of osteoporosis go	
CC	undetected at present.	
XX		
SQ	Sequence 2613 BP: 553 A; 750 C; 742 G; 568 T; 0 other:	
	Query Match	100.0%; Score 20; DB 21; Length 2613;
	Best Local Similarity	100.0%; Pred. No. 5.5;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AGGACTCTGAGGCTCTTCT 20	
DB	501 AGGACTCTGAGGCTCTTCT 520	
	RESULT 12	
	ABK83997	
XX	ABK83997 standard: cDNA: 3683 BP.	
XX		
AC	ABK83997:	
XX		
DT	14-AUG-2002 (first entry)	
XX		
DE	Human cDNA differentially expressed in granulocytic cells #568.	
XX		
KW	Human; ss; granulocytic cell; DNA chip; bacterial infection;	
KW	viral infection; parasitic infection; protozoal infection;	
KW	fungal infection; sterile inflammatory disease; psoriasis;	
KW	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;	
KW	cardiac reperfusion injury; renal reperfusion injury; ARDS;	
KW	adult respiratory distress syndrome; inflammatory bowel disease;	
KW	Crohn's disease; ulcerative colitis; periodontal disease;	
KW	granulocyte activation; chronic inflammation; allergy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200228999-A2.	
XX		
PD	11-APR-2002.	
XX		
PF	03-OCT-2001; 2001WO-US30821.	

XX 03-OCT-2000; 2000US-237189P.
PR (GENE-) GENE LOGIC INC.
XX
PA
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI: 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID NO 568; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA; preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g., psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC http://wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other:
XX
Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY 1 AGCACTCGAGCCTCTTCT 20
XXXXXXXXXXXXXXXXXXXX
Db 1571 AGGACTGTGAGGCTCTTCT 1590
XX
RESULT 13
ABL65877
XX ABL65877 standard; DNA; 3683 BP.
XX
AC ABL65877;
XX
XX
XX 15-MAY-2002 (first entry)
XX
XX Lung cancer related gene sequence SEQ ID NO:4214.
DE

XX	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cystostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma
KM	gens; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-AZ.
XX	
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US10838.
XX	
PR	05-JUN-2000; 2000US-209473P.
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-233617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234509P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
PR	25-SEP-2000; 2000US-234924P.
PR	25-SEP-2000; 2000US-235077P.
PR	25-SEP-2000; 2000US-235082P.
PR	25-SEP-2000; 2000US-235134P.
PR	25-SEP-2000; 2000US-235280P.
PR	26-SEP-2000; 2000US-235637P.
PR	26-SEP-2000; 2000US-235638P.
PR	27-SEP-2000; 2000US-235711P.
PR	27-SEP-2000; 2000US-235720P.
PR	27-SEP-2000; 2000US-235840P.
PR	27-SEP-2000; 2000US-235863P.
PR	28-SEP-2000; 2000US-236028P.
PR	28-SEP-2000; 2000US-236032P.
PR	28-SEP-2000; 2000US-236033P.
PR	28-SEP-2000; 2000US-236034P.
PR	28-SEP-2000; 2000US-236109P.
PR	28-SEP-2000; 2000US-236111P.
PR	29-SEP-2000; 2000US-236842P.
PR	29-SEP-2000; 2000US-236891P.
PR	02-OCT-2000; 2000US-237172P.
PR	02-OCT-2000; 2000US-237173P.
PR	02-OCT-2000; 2000US-237278P.
PR	02-OCT-2000; 2000US-237294P.
PR	02-OCT-2000; 2000US-237295P.
PR	02-OCT-2000; 2000US-237316P.
PR	03-OCT-2000; 2000US-237425P.
PR	03-OCT-2000; 2000US-237598P.
PR	03-OCT-2000; 2000US-237604P.
PR	03-OCT-2000; 2000US-237606P.
PR	03-OCT-2000; 2000US-237608P.
PR	01-NOV-2000; 2000US-244867P.
PR	01-NOV-2000; 2000US-245084P.
XX	
PA	(AVALON PHARM.
XX	
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI	Soppet DR, Weaver Z;
XX	
DR	WPI: 2002-188264/24.
XX	
PT	Screening for anti-neoplastic agent involves exposing cells to a
PT	chemical agent to be tested for anti-neoplastic activity, and
XX	determining a change in expression of a gene of a signature gene set
PS	Claim 1; SEQ ID 4214; 44pp; English.
XX	
CC	The present invention describes a method (M1) for screening for an
CC	anti-neoplastic agent. The method involves exposing cells to a chemical
CC	agent to be tested for anti-neoplastic activity, determining a change in

expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 3683 BP: 781 A: 1098 C: 1086 G: 718 T: 0 other:

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGGACTCTGAGGCTCTTCT 20
1571 AGGACTCTGAGGCTCTTCT 1590

RESULT 14

ABK33465
ID ABK33465 standard; DNA: 3683 BP.

AC ABK33465;

DT 23-APR-2002 (first entry)

DE Human TNF receptor II gene.

XX Human: anti-tumour necrosis factor receptor II; TNF receptor II;

KW Chromosome 1p36; Infliximab therapy; Crohn's disease; malignant disorder;

KW Inflammatory disorder; chronic disease; receptor; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 90..1475

FT /*tag= a

FT /product= "TNF receptor II"

FT sig_peptide 90..155

FT /*tag= b

FT mat_peptide 156..1472

FT /*tag= c

FT EP1172444-A1.

PN 16-JAN-2002.

PD 10-JUL-2000; 2000EP-0114786.

PF 10-JUL-2000; 2000EP-0114786.

PR 10-JUL-2000; 2000EP-0114786.

XX (CONA-) CONARIS RES INST GMBH.

XX Schreiber S, Hampe J, Mascheretti S;

XX WPI: 2002-156651/21.

DR P-PSDB: AAU75172.

XX Detecting non-responders to anti-human necrosis factor therapy,

XX comprises testing an individual for homozygosity for a single

XX nucleotide polymorphism in the gene coding for the tumour necrosis

XX factor receptor II -

XX Disclosure: Page 23-27; 45pp; English.

The present invention relates to a method for detecting non-responders to anti-tumour necrosis factor (TNF) therapy. The method involves testing an individual for homozygosity for at least one single nucleotide polymorphism (SNP) in the gene coding for TNF receptor II, which is located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168 A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and Met196Arg respectively, are also described. The method of the invention is useful for detecting non-responders to anti-TNF therapy such as infliximab therapy, or therapy of Crohn's disease. The genes containing the 2 novel polymorphisms are useful for diagnostic purposes in inflammatory, malignant or other chronic diseases. The present sequence encodes for human TNF receptor II.

Sequence 3683 BP: 781 A: 1098 C: 1086 G: 718 T: 0 other:

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGGACTCTGAGGCTCTTCT 20
1571 AGGACTCTGAGGCTCTTCT 1590

RESULT 15

ABK33466
ID ABK33466 standard; DNA: 3683 BP.

AC ABK33466;

DT 23-APR-2002 (first entry)

DE Human TNF receptor II gene with SNP in exon 2.

XX Human: anti-tumour necrosis factor receptor II; TNF receptor II; SNP;

KW Chromosome 1p36; Infliximab therapy; Crohn's disease; malignant disorder;

KW Inflammatory disorder; chronic disease; receptor; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 90..1475

FT /*tag= a

FT /product= "TNF receptor II variant #1"

FT sig_peptide 90..155

FT /*tag= b

FT mat_peptide 156..1472

FT /*tag= c

FT variation replace (257, A)

FT /*tag= d

FT standard_name= "Single nucleotide polymorphism"

FT EP1172444-A1.

PN 16-JAN-2002.

PD 10-JUL-2000; 2000EP-0114786.

PF 10-JUL-2000; 2000EP-0114786.

PR 10-JUL-2000; 2000EP-0114786.

XX (CONA-) CONARIS RES INST GMBH.

XX Schreiber S, Hampe J, Mascheretti S;

XX WPI: 2002-156651/21.

DR P-PSDB: AAU75173.

XX Detecting non-responders to anti-human necrosis factor therapy,

XX comprises testing an individual for homozygosity for a single

XX nucleotide polymorphism in the gene coding for the tumour necrosis

XX factor receptor II -

PS Claim 15; Page 29-33; 45pp; English.

XX The present invention relates to a method for detecting non-responders
 CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
 CC an individual for homozygosity for at least one single nucleotide
 CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
 CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
 CC A/C) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
 CC Met196Arg respectively, are also described. The method of the invention
 CC is useful for detecting non-responders to anti-TNF therapy such as
 CC Infliximab therapy, or therapy of Crohn's disease. The genes containing
 CC the 2 novel polymorphisms are useful for diagnostic purposes in
 CC inflammatory, malignant or other chronic diseases. The present sequence
 CC represents the human TNF receptor II gene containing the SNP in exon 2.

XX
 SQ Sequence 3683 BP: 780 A; 1098 C; 1087 G; 718 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3683;

Best Local Similarity 100.0%; Pred. No. 5.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTTCT 20

|||||

ub 1571 AGGACTCTGAGGCTTCT 1590

Search completed: December 5, 2002, 23:30:05
 Job time : 9.80891 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 ; Search time 38.2783 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937A-4
Perfect score: 20
Sequence: 1 agagctctgagctcttct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estcpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	150	10	AM176594 RC5-CT007
2	20	100.0	372	9	AA031826 zk14b1.r
3	20	100.0	760	13	B1161017 B1161017
4	20	100.0	827	12	BF347834 BF347834
5	20	100.0	845	13	B1160187 B1160187
6	20	100.0	932	12	BC829828 BC829828

7	20	100.0	1051	12	BF568409	BF568409	602184408
c	8	20	100.0	1053	14	BO052282	AGENCOURT
9	20	100.0	1066	12	BF568708	BF568708	602184353
10	20	100.0	1102	14	BM317316	BM317316	AGENCOURT
11	20	100.0	2291	11	BC011844	BC011844	Hom sapi
12	18.4	92.0	175	10	AM062603	AM062603	RC0-CT008
c	13	18.4	92.0	602	17	AG129979	Pan trogl
c	14	18	90.0	562	12	AZ803826	2M0064319
c	15	18	90.0	682	17	BC504723	602551929
16	18	90.0	942	12	BC398850	BC398850	602440491
17	18	90.0	1024	12	BC330670	BC330670	602560073
18	17.4	87.0	469	13	BM330983	BM330983	f99b08.y
c	19	17.4	613	10	BB635291	BB635291	BB635291
c	20	17.4	637	14	BO259709	BO259709	faa03b08.
c	21	17.4	683	10	BE557682	BE557682	fl13a11.y
c	22	17.4	686	9	AI658162	AI658162	fc19e09.y
c	23	17.4	713	13	B1888410	B1888410	zF637-2.0
24	17	85.0	410	9	AI249361	AI249361	qx53e12.x
25	17	85.0	468	14	W38599	W38599	zbi19f10.r1
26	17	85.0	556	17	BM358756	BM358756	CH230-163
27	17	85.0	562	12	BF666770	BF666770	602121274
28	17	85.0	639	12	BC668518	BC668518	602510494
29	17	85.0	647	17	BM304119	BM304119	CH230-4C3
30	17	85.0	687	12	BC572056	BC572056	602592525
31	17	85.0	763	13	B1916547	B1916547	603178457
32	17	85.0	794	17	BH052157	BH052157	RPCI-24-3
33	16.8	84.0	206	9	AI874007	AI874007	wm47b01.x
c	34	16.8	212	12	BF094241	BF094241	CM1-UT004
35	16.8	84.0	267	10	BB092178	BB092178	EST263522
c	36	16.8	281	9	AI782643	AI782643	UI-E-E01-
37	16.8	84.0	281	14	BM682190	BM682190	601769216
c	38	16.8	282	14	BM729280	BM729280	601769216
c	39	16.8	299	12	BF162756	BF162756	EST263523
c	40	16.8	313	9	AI782644	AI782644	ux47c12.y
41	16.8	84.0	320	12	BG277660	BG277660	tq48f09.x
42	16.8	84.0	327	9	AI561366	AI561366	zc66a05.r1
c	43	16.8	336	14	W32334	W32334	zP24d03.r
c	44	16.8	361	9	AA172113	AA172113	ux47c12.x
c	45	16.8	364	12	BG228078	BG228078	

ALIGNMENTS

RESULT 1
AM176594
LOCUS
DEFINITION
RC5-CT0070-200899-001-H12 CT0070 Homo sapiens CDNA, mRNA sequence.
ACCESSION
AM176594
VERSION
AM176594.1 GI:6442631
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS
1 (bases 1 to 150)
TITLE
HCGP <http://www.ludwig.org.br/ORESTES>.
JOURNAL
The FAPESP/LICR Human Cancer Genome Project
COMMENT
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&t2=RC5-CT0070-200899-001-H12&t3=1999-08-20&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 150.

RESULT 4
BF347834 827 bp mRNA linear EST 22-NOV-2000
LOCUS 602022970F1 NCL_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4158473
DEFINITION 5', mRNA sequence.
ACCESSION BF347834
VERSION BF347834.1 GI:11295429
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 827)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9434 row: k column: 18
High quality sequence stop: 721.
Location/Qualifiers
1..827
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4158473"
/clone_lib="NCL_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (71 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPOrt6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP Library."

BASE COUNT 160 a 253 c 273 g 141 t

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 827;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTCTGAGCTCTTCT 20
|||||
Db 653 AGGACTCTGAGCTCTTCT 672

RESULT 5
B1160187 845 bp mRNA linear EST 05-JUL-2001
LOCUS 602864057F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:5018007 5',
DEFINITION mRNA sequence.
ACCESSION B1160187
VERSION B1160187.1 GI:14620188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 845)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1831 row: a column: 16
High quality sequence stop: 845.
Location/Qualifiers
1..845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5018007"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOT87; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAGC. Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. 1"

BASE COUNT 147 a 258 c 261 g 179 t

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 845;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGCTCTTCT 20
|||||
Db 633 AGGACTCTGAGCTCTTCT 652

RESULT 6
BG829828 932 bp mRNA linear EST 22-MAY-2001
LOCUS 602764119F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:4899436 5',
DEFINITION mRNA sequence.
ACCESSION BG829828
VERSION BG829828.1 GI:14177415
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1791 row: e column: 05
High quality sequence stop: 833.
Location/Qualifiers
1..932
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4899436"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOT87; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library. 1"

BASE COUNT 162 a 296 c 296 g 177 t 1 others
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 932;
Best Local Similarity 100.0%; Pred. No. 57;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGCTCTTTCT 20
|||||

Db 593 AGGACTGTGAGCTCTTTCT 612

RESULT 7

BF568409

LOCUS 60218440BF1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300633 5',
DEFINITION mRNA sequence.

ACCESSION BF568409

VERSION BF568409.1 GI:11641789

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

1 (bases 1 to 1051)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://Image.llnl.gov

Plate: L16M1159 row: c column: 02

High quality sequence stop: 769.

Location/Qualifiers

1..1051

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4300633"

/clone_lib="NIH_MGC_42"

/tissue_type="epithelioid carcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; CDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH-MGC Library. 1"

BASE COUNT 229 a 313 c 346 g 161 t 2 others

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 1051;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGCTCTTTCT 20
|||||

Db 592 AGGACTGTGAGCTCTTTCT 611

RESULT 8
BQ052282/c 1053 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT 6868457 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935311
DEFINITION 5', mRNA sequence.

BASE COUNT BQ052282 1 GI:19811622

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 1053;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGCTCTTTCT 20
|||||

Db 826 AGGACTGTGAGCTCTTTCT 807

RESULT 9

BF568708

LOCUS 602184353F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 5',
DEFINITION mRNA sequence.

ACCESSION BF568708

VERSION BF568708.1 GI:11642088

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

1 (bases 1 to 1053)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/MCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://Image.llnl.gov

Plate: L16M2118 row: c column: 16

High quality sequence stop: 649.

Location/Qualifiers

1..1053

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5935311"

/clone_lib="NIH_MGC_106"

/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; CDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH-MGC Library."

BASE COUNT 216 a 328 c 297 g 212 t

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 1053;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGCTCTTTCT 20
|||||

Db 826 AGGACTGTGAGCTCTTTCT 807

RESULT 9

BF568708

LOCUS 602184353F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 5',
DEFINITION mRNA sequence.

ACCESSION BF568708

VERSION BF568708.1 GI:11642088

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

1 (bases 1 to 1066)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LNCM1159 row: 1 column: 13
 High quality sequence stop: 712.

FEATURES

source

1. 1066

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4300500"

/clone_1lb="NIH_MGC_42"

/tissue_type="epithelioid carcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GCGACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. |"

BASE COUNT

ORIGIN

216 a 316 c 354 g 180 t

Query Match

100.0%; Score 20; DB 12; Length 1066;

Best Local Similarity

100.0%; Pred. NO. 60;

Matches

20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AGACTCTGAGCCTCTTCT 20

|||||

Db 477 AGACTCTGAGCCTCTTCT 496

RESULT 10

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 1102

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5483819"

/clone_1lb="NIH_MGC_106"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

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/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

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/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GCGACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

BASE COUNT

ORIGIN

219 a 366 c 292 g 222 t 3 others

Query Match

100.0%; Score 20; DB 14; Length 1102;

Best Local Similarity

100.0%; Pred. NO. 61;

Matches

20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AGACTCTGAGCCTCTTCT 20

|||||

Db 93 AGACTCTGAGCCTCTTCT 112

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 2291

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4111730"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

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/tissue_type="muscle, rhabdomyosarcoma"

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/tissue_type="muscle, rhabdomyosarcoma"

/tissue_type="muscle, rhabdomyosarcoma"

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Caltech, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nsl.nih.gov

Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,

Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-U., Karlins, E., Legaspi, R.,

Lim, M., Maduro, Q.U., Mastello, C., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Snyder, B., Stantrop, S., Thomas, P.J.,

Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,

Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>

Series: IRAL Plate: 28 Row: 1 Column: 15

This clone was selected for full length sequencing because it

passed the following selection criteria: Similarity but not

identity to protein

This clone has the following problem: incomplete processing.

FEATURES

source

1. 2291

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4111730"

/tissue_type="muscle, rhabdomyosarcoma"

clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

BASE COUNT 461 a 708 c 713 g 409 t

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 2291;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGCCTCTTCT 20
|||||

Db 1480 AGGACTCTGAGCCTCTTCT 1499

RESULT 12
AM062603

LOCUS AM062603 175 bp mRNA linear EST 06-OCT-1999
DEFINITION RC0-CT0088-050899-001-B07 CT0088 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM062603
VERSION AM062603.1 GI:6013988
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 175)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC0-CT0088-050899-001-B07&f3=1999-08-05&f4=1>)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 175.
Location/Qualifiers
1..175
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0088"
/dev_stage="Adult"
/note="Organ: Colon; Vector: pUC18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 32 a 65 c 46 g 32 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 175;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGCCTCTTCT 20
|||||

Db 66 AGGACTCTGAGCCTCTTCT 85

RESULT 13
AG129979/c

LOCUS AG129979 602 bp DNA linear GSS 04-NOV-2001

DEFINITION Pan troglodytes DNA, clone: PTB-14J18.F, genomic survey sequence.
ACCESSION AG129979
VERSION AG129979.1 GI:16659144
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC library clone:PTB-14J18.F.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
2 (bases 1 to 602)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
DIRECT SUBMISSION
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpses@sc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB this BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..602
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-14J18.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 154 a 143 c 101 g 204 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 17; Length 602;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGCCTCTTCT 20
|||||

Db 465 AGGACTCTGAGCCTCTTGT 446

RESULT 14
AZ803826/c

LOCUS AZ803826 562 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0064J19F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUCG2M0064J19 F, DNA sequence.
ACCESSION AZ803826
VERSION AZ803826.1 GI:12956149
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 562)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0064 row: J column: 19
 Seq primer: CGTTGTAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 562.
 Location/Qualifiers

FEATURES

source

1..562
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0064J19"
 /clone_lib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

191 a 104 c 116 g 151 t

ORIGIN

Query Match 90.0%; Score 18; DB 17; Length 562;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACTCTGAGGCTCTTCT 20
 ||||||||||||||||
 Db 395 GACTCTGAGGCTCTTCT 378

RESULT 15

BG504723

LOCUS

602551929F1 NIH_MGC_61 Homo sapiens cDNA IMAGE:4664527 5',

DEFINITION

ACCESSION

BG504723

KEYWORDS

EST.

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.C.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.C.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10M1468 row: 1 column: 08
 High quality sequence stop: 628.
 Location/Qualifiers

FEATURES

source

1..682
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4664527"
 /clone_lib="NIH_MGC_61"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
 Site1 (ggccgctcgcc); Site_2: Site1 (ggccatattggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor
 sequence: 5'-ATTCTGAGAGCCGAGCGCGCCGACATG-dT(30)BR-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 Library."

BASE COUNT

226 a 141 c 164 g 151 t

ORIGIN

Query Match 90.0%; Score 18; DB 12; Length 682;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACTCTGAGGCTCTTTC 19
 ||||||||||||||||
 Db 1 GGACTCTGAGGCTCTTTC 18

Search completed: December 6, 2002, 04:54:31
 Job time : 50.2783 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 : Search time 1.03896 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-4

Sequence: 1 agagctcagagctcttct 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PCNUS.COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	1641	1 US-08-385-229-1	Sequence 1, Appl
2	20	100.0	1641	2 US-08-650-000-1	Sequence 1, Appl
3	20	100.0	1641	6 5395760-1	Patent No. 5395760
4	20	100.0	2224	4 US-08-477-347-2	Sequence 2, Appl
5	20	100.0	2224	4 US-08-476-862-1	Sequence 1, Appl
6	20	100.0	3683	4 US-09-844-634-3	Sequence 3, Appl
7	20	100.0	15602	4 US-09-844-634-3	Sequence 17, Appl
8	16	80.0	1318	5 PCT-US94-07127A-1	Sequence 1, Appl
9	16	80.0	1336	4 US-09-257-179-13	Sequence 13, Appl
10	15.8	79.0	2064	3 US-08-875-944B-1	Sequence 1, Appl
11	15.8	79.0	2064	4 US-09-116-049-3	Sequence 3, Appl
12	15.8	79.0	98844	4 US-09-791-211-10	Sequence 10, Appl
13	15.2	76.0	321	2 US-08-232-081B-35	Sequence 35, Appl
14	15.2	76.0	321	2 US-08-232-081B-35	Sequence 35, Appl
15	15.2	76.0	678	4 US-09-605-785-605	Sequence 605, App
16	15.2	76.0	678	4 US-09-605-785-605	Sequence 604, App
17	15.2	76.0	694	4 US-09-605-785-604	Sequence 604, App
18	15.2	76.0	694	4 US-09-605-785-604	Sequence 665, App
19	15.2	76.0	705	4 US-09-605-785-665	Sequence 665, App
20	15.2	76.0	817	4 US-09-605-785-603	Sequence 603, App
21	15.2	76.0	817	4 US-09-605-785-603	Sequence 667, App
22	15.2	76.0	854	4 US-09-247-155-67	Sequence 67, App
23	15.2	76.0	1488	2 US-08-687-559-5	Sequence 5, Appl
24	15.2	76.0	1805	4 US-08-961-527-247	Sequence 247, App
25	15.2	76.0	5599	2 US-08-477-451-9	Sequence 9, Appl
26	15.2	76.0	5599	2 US-08-477-451-13	Sequence 13, Appl
27	15.2	76.0	9495	1 US-08-271-829-1	Sequence 1, Appl

C 28	15.2	76.0	9495	5 PCT-US93-01544-1	Sequence 1, Appl
C 29	15.2	76.0	19932	2 US-08-477-451-25	Sequence 25, Appl
C 30	14.8	74.0	639	1 US-08-480-784-26	Sequence 26, Appl
C 31	14.8	74.0	639	1 US-08-483-553-26	Sequence 26, Appl
C 32	14.8	74.0	639	1 US-08-487-002-26	Sequence 26, Appl
C 33	14.8	74.0	639	1 US-08-483-554B-26	Sequence 26, Appl
C 34	14.8	74.0	639	1 US-08-488-011B-26	Sequence 26, Appl
C 35	14.8	74.0	639	4 US-08-850-727-26	Sequence 26, Appl
C 36	14.8	74.0	639	5 PCT-US95-10202-26	Sequence 26, Appl
C 37	14.8	74.0	639	5 PCT-US95-10203-26	Sequence 26, Appl
C 38	14.8	74.0	639	5 PCT-US95-10203-26	Sequence 26, Appl
C 39	14.8	74.0	646	4 US-09-222-575-79	Sequence 26, Appl
C 40	14.8	74.0	2492	3 US-08-695-191-3	Sequence 26, Appl
C 41	14.8	74.0	2492	3 US-08-682-080-3	Sequence 3, Appl
C 42	14.8	74.0	3227	4 US-09-221-017B-451	Sequence 451, App
C 43	14.8	74.0	4041	1 US-08-147-812-4	Sequence 4, Appl
C 44	14.8	74.0	4110	3 US-09-123-708-1	Sequence 1, Appl
C 45	14.8	74.0	4110	3 US-09-123-624-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-385-229-1
: Sequence 1, Application US/08385229
: Patent No: 5605690
GENERAL INFORMATION:
: APPLICANT: Jacobs, Cindy A.
: APPLICANT: Smith, Craig A.
: TITLE OF INVENTION: Method of Treating TNF-Dependent
: TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
: NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: U.S.A.
: ZIP: 98101
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/385,229
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/946,236
: FILING DATE:
ATTORNEY/AGENT INFORMATION:
: NAME: Wright, Christopher L.
: REGISTRATION NUMBER: 31,680
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1641 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: Fibroblast
: CELL LINE: WI-26 VAA
: IMMEDIATE SOURCE:

LIBRARY: WI-26 VA4
CLONE: Clone 1
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1473
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 154..1470
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 88..153
US-08-385-229-1

Query Match 100.0%; Score 20; DB 1; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGGCTCTTCT 20
Db 1569 AGGACTGTGAGGCTCTTCT 1588

RESULT 2
US-08-650-000-1
Sequence 1, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: MIGHT, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: WI-26 VA4
IMMEDIATE SOURCE:
LIBRARY: WI-26 VA4
CLONE: 1
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1473
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 154..1470
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 88..153
PUBLICATION INFORMATION:
AUTHORS: Smith, Craig A.
AUTHORS: Davis, Terri
AUTHORS: Anderson, Dirk
AUTHORS: Solam, Lisabeth
AUTHORS: Beckmann, M. P.
AUTHORS: Jerzy, Rita
AUTHORS: Dower, Steven K.
AUTHORS: Cosman, David
AUTHORS: Goodwin, Raymond G.
TITLE: A Receptor for Tumor Necrosis Factor Defines
TITLE: an Unusual Family of Cellular and Viral Proteins
JOURNAL: Science
VOLUME: 248
PAGES: 1019-1023
DATE: 25-MAY-1990
US-08-650-000-1

Query Match 100.0%; Score 20; DB 2; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGGCTCTTCT 20
Db 1569 AGGACTGTGAGGCTCTTCT 1588

RESULT 3
5395760-1
Patent No. 5395760
APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN, M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ. ID NO: 1:
LENGTH: 1641
5395760-1

Query Match 100.0%; Score 20; DB 6; Length 1641;

Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTCTGAGGCTCTTCT 20
|||||
Db 1569 AGACTCTGAGGCTCTTCT 1588

RESULT 4
US-08-477-347-2

Sequence 2, Application US/08477347
Patent No. 6232446
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,665
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472
US-08-477-347-2

Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTCTGAGGCTCTTCT 20
|||||
Db 1571 AGACTCTGAGGCTCTTCT 1590

RESULT 5
US-08-476-862-1
Sequence 1, Application US/08476862

Patent No. 6262239
GENERAL INFORMATION:

APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472
US-08-476-862-1

Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTCTGAGGCTCTTCT 20
|||||
Db 1571 AGACTCTGAGGCTCTTCT 1590

RESULT 6
US-09-844-634-3
Sequence 3, Application US/09844634
Patent No. 6410324

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRE

```
FILE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 3
LENGTH: 3683
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)...(1475)
US-09-844-634-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 3683;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTGTGAGGCTCTTCT 20
DB 1571 AGACTGTGAGGCTCTTCT 1590

RESULT 7
US-09-844-634-17
Sequence 17, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Walt
FILE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSION
TITLE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 17
LENGTH: 15602
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-844-634-17

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 15602;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTGTGAGGCTCTTCT 20
DB 11104 AGACTGTGAGGCTCTTCT 11123

RESULT 8
PCT-US94-07127A-1
Sequence 1, Application PC/TUS9407127A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, an
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCH, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07127A
FILING DATE: submitted herewith
```

```
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-184
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US94-07127A-1

Query Match
Best Local Similarity 80.0%; Score 16; DB 5; Length 1318;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ACTCTGAGGCTCTTC 19
DB 12 ACTCTGAGGCTCTTC 27

RESULT 9
US-09-257-179-13/C
Sequence 13, Application US/09257179
Patent No. 6410709
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/257,179
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US98/17709
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 60/056,270
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,247
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,073
EARLIER FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 1336
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (766)
OTHER INFORMATION: n equals a,t,g, or c
US-09-257-179-13

Query Match
Best Local Similarity 80.0%; Score 16; DB 4; Length 1336;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGACTGTGAGGCTCTTCT 20
DB 232 AGGATYTTGAGGCTGTCT 213

RESULT 10
US-08-875-944B-1/C
Sequence 1, Application US/08875944B
```

Patent No. 6096542
GENERAL INFORMATION:
APPLICANT: FUJINAGA, Kei
APPLICANT: YOSHIDA, Koichi
APPLICANT: HIGASHINO, Fumihito
TITLE OF INVENTION: CANCER CONTROL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,944B
FILING DATE: 07-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 07-020173
FILING DATE: 08-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00016
FILING DATE: 09-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FUJINAGA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1386
US-08-875-944B-1

Query Match 79.0%; Score 15.8; DB 3; Length 2064;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACTCTGAGGCTCTTCT 20
||||| ||||| ||||| |||||
DB 239 GGACTCTGGGCTCTTCT 221

RESULT 11
US-09-116-049-3/C
Sequence 3, Application US/09116049A
Patent No. 6248351
GENERAL INFORMATION:
APPLICANT: Hung, Men-Chie
TITLE OF INVENTION: HUMAN PEAK IS A TUMOR SUPPRESSOR FOR CANCER CELLS
FILE REFERENCE: UTSC:582
CURRENT APPLICATION NUMBER: US/09/116,049A
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2064
TYPE: DNA
ORGANISM: Homo sapiens

US-09-116-049-3
Query Match 79.0%; Score 15.8; DB 4; Length 2064;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACTCTGAGGCTCTTCT 20
||||| ||||| ||||| |||||
DB 239 GGACTCTGGGCTCTTCT 221

RESULT 12
US-09-791-211-10
Sequence 10, Application US/09791211
Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 98844
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 24962
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 64383
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65468
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65469
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 87130
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 89049
OTHER INFORMATION: unknown
OTHER INFORMATION: unknown
US-09-791-211-10

Query Match 79.0%; Score 15.8; DB 4; Length 98844;
Best Local Similarity 89.5%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTC 19
||| | ||||| ||||| |||||
DB 41628 AGGCACTGAGGCTCTTTC 41646

RESULT 13
US-08-232-081B-35/C
Sequence 35, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HINOSHI

```
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-232-081B-35

Query Match          76.0%  Score 15.2;  DB 2;  Length 321;
Best Local Similarity 85.0%  Pred. No. 71;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGACTCTGAGGCTCTTCT 20
    ||||| || ||||| |||||
Db 67 AGCAGCTGTGCGCTTCT 48

RESULT 14
US-08-232-081B-36/C
; Sequence 36, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
```

```
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-232-081B-36

Query Match          76.0%  Score 15.2;  DB 2;  Length 321;
Best Local Similarity 85.0%  Pred. No. 71;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 1 AGACTCTGAGGCTCTTCT 20
    ||||| || ||||| |||||
Db 67 AGCAGCTGTGCGCTTCT 48
```

```
RESULT 15
US-09-605-785-605
; Sequence 605, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 605
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(678)
; OTHER INFORMATION: n = A,T,C or G
US-09-605-785-605
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Query Match          76.0%  Score 15.2;  DB 4;  Length 678;
Best Local Similarity 85.0%  Pred. No. 77;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGACTCTGAGGCTCTTCT 20
    ||||| ||||| ||||| |||||
Db 432 AGACTCTGTGCGCTTCT 451
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Search completed: December 5, 2002, 23:39:10
Job time : 34.039 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 20:03:23 Search time 0.972171 Seconds

(without alignments)
8021.899 Million cell updates/sec

Title: US-09-856-937a-4

Sequence: 1 aggaactctgagcctcttct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	1641	10	US-09-758-124-1 Sequence 1, Appl1
2	20	100.0	2224	10	US-09-800-909-1 Sequence 1, Appl1
3	20	100.0	2224	10	US-09-800-908-2 Sequence 2, Appl1
4	20	100.0	3683	10	US-09-954-456-1187 Sequence 1187, Ap
5	16.8	84.0	480	10	US-09-864-761-423 Sequence 423, App
6	16.8	84.0	580	10	US-09-867-701-6135 Sequence 6135, Ap
7	16.8	84.0	966	10	US-09-864-761-17222 Sequence 17222, A
8	16.8	84.0	1086	10	US-09-864-761-17120 Sequence 17120, A
9	16.8	84.0	1086	10	US-09-864-761-17617 Sequence 17617, A
10	16	80.0	526	10	US-09-864-761-12705 Sequence 12705, A
11	16	80.0	1336	10	US-09-729-835-13 Sequence 13, Appl1
12	15.8	79.0	239	9	US-10-002-344A-72 Sequence 72, Appl1
13	15.8	79.0	333	9	US-10-002-344A-73 Sequence 73, Appl1
14	15.8	79.0	527	10	US-09-867-550-1063 Sequence 1063, Ap
15	15.8	79.0	527	10	US-09-867-550-2118 Sequence 2118, Ap
16	15.8	79.0	2333	10	US-09-920-300A-1788 Sequence 1788, Ap
17	15.8	79.0	2333	10	US-09-880-107-3316 Sequence 3316, Ap
18	15.8	79.0	2333	12	US-10-033-528-1788 Sequence 1788, Ap
19	15.4	77.0	433	10	US-09-867-701-10530 Sequence 10530, A

20	15.4	77.0	582	10	US-09-864-761-9755 Sequence 9755, Ap
21	15.2	76.0	248	10	US-09-983-965-3631 Sequence 3631, Ap
22	15.2	76.0	275	10	US-09-783-590-728 Sequence 728, App
23	15.2	76.0	300	10	US-09-815-242-9225 Sequence 9225, Ap
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26	15.2	76.0	438	10	US-09-960-352-12682 Sequence 12682, A
27	15.2	76.0	515	10	US-09-777-564-81 Sequence 81, Appl1
28	15.2	76.0	549	10	US-09-864-761-7389 Sequence 7389, Ap
29	15.2	76.0	590	10	US-09-777-564-543 Sequence 543, App
30	15.2	76.0	615	10	US-09-777-564-25 Sequence 25, Appl1
31	15.2	76.0	678	10	US-09-759-143-605 Sequence 605, App
32	15.2	76.0	678	10	US-09-759-143-664 Sequence 664, App
33	15.2	76.0	678	10	US-09-759-143-665 Sequence 665, App
34	15.2	76.0	678	10	US-09-780-669-605 Sequence 605, App
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ALIGNMENTS

RESULT 1
US-09-758-124-1
Sequence 1, Application US/09758124
Patent No. US20020006391A1
GENERAL INFORMATION:
APPLICANT: SMITH, Craig A.
APPLICANT: GOODMAN, Raymond G.
APPLICANT: BECKMANN, M. Patricia
TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
FILE REFERENCE: A7895
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 08/953,268
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 08/555,629
PRIOR FILING DATE: 1995-11-09
PRIOR APPLICATION NUMBER: 08/468,453
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/038,765
PRIOR FILING DATE: 1993-03-13
PRIOR APPLICATION NUMBER: 07/523,635
PRIOR FILING DATE: 1990-05-10
PRIOR APPLICATION NUMBER: 07/421,417
PRIOR FILING DATE: 1989-10-13
PRIOR APPLICATION NUMBER: 07/405,370
PRIOR FILING DATE: 1989-09-11
PRIOR APPLICATION NUMBER: 07/403,241
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1641
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (88)..(1473)
NAME/KEY: mat_peptide
LOCATION: (154)..(1470)
NAME/KEY: sig_peptide
LOCATION: (88)..(153)
US-09-758-124-1

7/11 Dec 6 10:02:27 2002

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Q	1717	CCCACTTCCCACCTTCAATTTCTCGGGGGCCCCAAACGGGGTGGCCCTGCCACTTTGGTACAG	1777
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Q	1777	GCCAGTGTGATCCCAAGTGGCAGCTCTTGTGTGCTGCTCTGTGTGGTGTCTGTGGTGTG	1831
D	2847	GCCAGTGTGATCCCAAGTGGCAGCTCTTGTGTGCTGCTCTGTGTGGTGTCTGTGGTGTG	2900
Q	1837	TGTAGCCAAAGTCGGTAACTTGAATGGCCCTGTGAAGCCACTGAAGCTGGGATTCCTC	1899
D	2907	TGTAGCCAAAGTCGGTAACTTGAATGGCCCTGTGAAGCCACTGAAGCTGGGATTCCTC	2966
Q	1897	CCCACTTGAATCAGACCTTCCCCCTCCACGGGGCCAGGGGCCCTGACAGAGGGGAAACAGTGT	1955
D	2967	CCCACTTGAATCAGACCTTCCCCCTCCACGGGGCCAGGGGCCCTGACAGAGGGGAAACAGTGT	3022
Q	1957	AGCCTTACCCGGATTTCTGGGAGGAAGCAGGTTTGAAGGGCTCTGTGAAGAGCTCAGTCTCA	2011
D	3027	AGCCTTACCCGGATTTCTGGGAGGAAGCAGGTTTGAAGGGCTCTGTGAAGAGCTCAGTCTCA	3088
Q	2017	GGAGCATGGGGATTAAGAGAGAGCATGAATTTGTCTAGACAGCAGGGGCGACGGGTGATA	2077
D	3087	GGAGCATGGGGATTAAGAGAGAGCATGAATTTGTCTAGACAGCAGGGGCGACGGGTGATA	3144
Q	2077	AATTGTTGATTAATTCACACTGAGCTTGAAGCTTGGCAGCTGAACTATTGGAGGTGGGA	2133
D	3147	AATTGTTGATTAATTCACACTGAGCTTGAAGCTTGGCAGCTGAACTATTGGAGGTGGGA	3200
Q	2137	GCCACGACATTAACATGAGAGCAAGAGGGTTTCCACCCTGGAAATCAGATGCTCAGACT	2199
D	3207	GCCACGACATTAACATGAGAGCAAGAGGGTTTCCACCCTGGAAATCAGATGCTCAGACT	3266
Q	2197	GGCTGGCTGACAGTGTACCTGTGACCTGTACTCAGAGAGGCTGAGGGGAGGATCAGTGAAGCCC	2255
D	3267	GGCTGGCTGACAGTGTACCTGTGACCTGTACTCAGAGAGGCTGAGGGGAGGATCAGTGAAGCCC	3332
Q	2257	AGGAGTTTGAAGCTGACAGCGAGCTATGATCGCGCACTACCTCAGACCTGAGCAACAGA	2311
D	3337	AGGAGTTTGAAGCTGACAGCGAGCTATGATCGCGCACTACCTCAGACCTGAGCAACAGA	3388
Q	2317	GTGAGACCCCTCTCTTAAAGAAAAAAAGTCAAGACTGCTGGGACTGGCCAGGTTCTTG	2377
D	3387	GTGAGACCCCTCTCTTAAAGAAAAAAAGTCAAGACTGCTGGGACTGGCCAGGTTCTTG	3444
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Q	2437	GGGAGAACCTCAGGCTTCTTGGCATCACAAGGCGAGCCGGGAAGCGATGAATTTGGAG	2499
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Q	2557	CACGTATGCTGGAGCGGATTCCTGCTTATCAATAAACCCTGTTGTTTAAAAAAA	2613
D	3627	CACGTATGCTGGAGCGGATTCCTGCTTATCAATAAACCCTGTTGTTTAAAAAAA	3683

RESULT 7
AAQ10956
ID AAQ10956 standard; DNA: 2339 BP.
~~XX~~
AC AAQ10956;

XX 24-MAY-1991 (first entry)
 XX Encodes human 75kD TNF-binding protein.
 DE Tumour Necrosis Factor; binding proteins; septic shock;
 KW autoimmune glomerulonephritis; lymphokine; cytokine..
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 XX Key Location/Qualifiers
 XX CDS 1..1179
 XX /tag=a
 XX /product= 75kD TNF-BP
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 XX EP417563-A.
 XX
 XX 20-MAR-1991.
 XX
 XX 31-AUG-1990; 90EP-0116707.
 XX
 XX 20-APR-1990; 90CH-0001347.
 XX 12-SEP-1989; 89CH-0003319.
 XX 08-MAR-1990; 90CH-0000746.
 XX
 XX (HOFF) HOFFMANN-LA ROCHE AG.
 XX
 XX Brochhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 XX Schlaeger EJ;
 XX WPI: 1991-081851/12.
 XX P-PSDB; AARI1605.
 XX
 XX Insoluble tumour necrosis factor binding proteins - and DNA
 XX encoding them, useful in pharmaceutical prods. and for antibody
 XX produ..
 XX
 XX Claim 4; Fig 1; 26pp; German.
 XX
 XX Partial amino acid sequences were determined for the 55 and 75kD
 XX TNF-BPs (see ARI1072-R11081) and oligonucleotide primers were
 XX synthesised based on these partial sequences. The primers were used
 XX to produce a cDNA fragment for use as a probe to screen a human
 XX placental cDNA bank constructed in lambda gtl1. Positive clones were
 XX identified and sequenced. Repeated sequencing showed a discrepancy
 XX at position 7 such that the third codon encodes either Thr or Ser.
 XX
 XX cDNA constructs comprising the TNF-BP coding sequence may also
 XX contain a fragment encoding a human Ig domain. Recombinant
 XX constructs are used to transform cells to confer improved TNF-
 XX binding properties.
 XX See also AAO10955.
 XX
 XX Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other;
 XX
 XX Query Match 54.5%; Score 1423; DB 12; Length 2339;
 XX Best Local Similarity 98.5%; Pred. No. 0;
 XX Matches 1457; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

Db 1103 CAGAGACCTGCTGGGAGACCGAAGAGAGCCCTGCTGCTTGGATGCTGATGCTG 1162
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 QY 389 GATGAAGCCCACTTAACCAAGCGCGGTGTGGCTGTGTGTGATGCCAAGGTGGGCTAGACC 448
 |||||||
 Db 1163 GATGAAGCCCACTTAACCAAGCGCGGTGTGGCTGTGTGTGATGCCAAGGT -GGCTAGACC 1221
 |||||||
 QY 449 CTGGCAGATGACCTTCGCAAGAGGGCCCTGTCTTCACAGGCCCCACACATAGACTCT 508
 |||||||
 Db 1222 CTGGCAGATGACCTTCGCAAGAGGGCCCTGTCTTCACAGGCCCCACACATAGACTCT 1281
 |||||||
 QY 509 GAGCCTCTTCTGGGCAAGTCTCTAGTCCCTCACAAGCCGAGCCCTGCTGTGACC 568
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 Db 1282 GAGCCTCTTCTGGGCAAGTCTCTAGTCCCTCACAAGCCGAGCCCTGCTGTGACC 1341
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 QY 569 TGCAGCCCAAGACAGAGCAGCAGAGTGGGGAAGCCTCTGTGCAATGATGTGTCCCT 628
 |||||||
 Db 1342 TGCAGCCCAAGACAGAGCAGCAGAGTGGGGAAGCCTCTGTGCAATGATGTGTCCCT 1401
 |||||||
 QY 629 CTGGGAAGGCTGGCTGGCATGACGTTCCGGGCAATGCTGGGCAAGTCCCTGACTCTCT 688
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 Db 1402 CTGGGAAGGCTGGCTGGCATGACGTTCCGGGCAATGCTGGGCAAGTCCCTGACTCTCT 1461
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 QY 689 GTGACCTGCCCCCGCCAGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 748
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 Db 1462 GTGACCTGCCCCCGCCAGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1521
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 QY 749 TTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 808
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 Db 1522 TTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1581
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 QY 809 GAAACCCCAACATCTTTTCTGCAAGAGGGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
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 Db 1582 GAAACCCCAACATCTTTTCTGCAAGAGGGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1641
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 QY 869 TCACCATGAAGACAGACAGACAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 928
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 QY 1229 GGTTCAGAGAGCCGAGATCAAGCCACTGCACTCCAGCTGGGGGAGACAGAGCAGAGTCT 1288
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 Db 2121 GGTGTGAAGTACAGATGCCAGAGAGGAGCCAGAGAGCCACCATATTCAGTCTGTGCTCT 2180
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 QY 1409 GGGCAAGATACGCACTTCAATCTGAATCTGCCAATTTTAAAAAAGTAACTACAC 1468
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Query Match	54.5%	Score 1423;	DB 20;	Length 2339,
Best Local Similarity	98.5%;	Pred. No. 0;		

[illegible]

GenCore version 5.1.3
Copyright (c) 1993 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:30:25 : Search time 5415.07 seconds

(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937A-1

Perfect score: 2613

Sequence: 1 tcttgctcgcgcctcgcgc.....ccgtttgttttaaaaaa 2613

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	2575	98.5	187877	2	AC023251
5	2493	95.4	3683	6	AX333705
6	2493	95.4	3683	6	AX338016
7	2493	95.4	3683	6	AX348018
8	2493	95.4	3683	6	AX348020
9	2493	95.4	3683	6	HUMNFR
10	2444.6	93.6	3492	9	S63368
11	2190	83.8	3380	11	G26865
12	1423	54.5	2339	6	A26415
13	1171	44.8	2394	9	HUMNFR11
14	1034	39.6	2224	6	AR152033
15	1034	39.6	2253	6	A78517
16	870	33.3	870	11	G15915
17	453	17.3	1641	6	I36196
18	443.8	17.0	480	9	AB030952
19	435.6	16.7	10950	9	HUMNFR2
20	337.8	12.9	435	6	AX198606
21	336	12.9	336	6	AX209144
22	323	12.4	1080	9	HUMNFR4
23	266	10.2	196423	2	AC116933
24	259.2	9.9	321519	2	AL714004
25	255.4	9.8	37680	2	AL359985
26	253.8	9.7	97385	2	HS0447F3
27	252.2	9.7	99688	2	AL831785_3
28	252.2	9.7	156143	2	AC128712
29	252.2	9.7	183338	2	AC069514
30	252.2	9.7	197078	2	AC117382
31	251.8	9.6	150970	2	AC120838
32	248.6	9.5	121826	9	AL354935
33	248.6	9.5	160038	9	AL138755
34	248.4	9.5	138532	2	AC004812
35	248.4	9.5	173213	2	AC073865
36	248.2	9.5	208024	9	AC010900
37	247.8	9.5	113964	9	AL589872
38	247.8	9.5	143981	9	HSJ1050K3
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ALIGNMENTS

RESULT 1
LOCUS HSTNFR2S10
DEFINITION Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 10 and complete cds.
ACCESSION U52165.1 GI:1469539
VERSION 1
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2613)
Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,

LePaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J., and Brodeur,G.M.
Physical mapping and genomic structure of the human TNFR2 gene
Genomics 35 (1), 94-100 (1996)
96299745
8661109

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

2 (bases 1 to 2613)
Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
LePaslier,D., Stallard,B.J., Goeddel,D.V., desauvage,F.J. and
Brodeur,G.M.

Direct Submission
Submitted (25-MAR-1996) Christian P. Beltinger, Division of
Oncology, ARC Rm. 902 D, Children's Hospital of Philadelphia, 324
South 34th Street, Philadelphia, PA 19104-4318, USA

FEATURES
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Location/Qualifiers

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Intron
exon
BASE COUNT
ORIGIN

553 a 750 c 742 g 568 t

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Best local Similarity 100.0%; Pred. No. 0;
Matches 2613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 601 AAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Oy      1741  GGGCCCAACAGGGGCTGCTCTGCTCTGATGATGGCCAGTGTGATGCCCAAGTCCAGT 1800
Db      1741  GGGCCCAACAGGGGCTGCTCTGCTCTGATGATGGCCAGTGTGATGCCCAAGTCCAGT 1800
Oy      1801  CTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
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Oy      2581  GCTTATCAATTAACCTTTTGTAAAAAAA 2613
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RESULT 2
 HS118D24/c
 LOCUS
 DEFINITION
 Human DNA sequence from clone 118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 like (pseudo)gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBP11, TNF R2, CD120B, TNFR). Contains ESTs, STSs, GSSs, genomic marker DIS434 and a ca repeat polymorphism, complete sequence.

ACCESSION
 AL031276.1 GI:3947780
 VERSION
 HTG: 60S Ribosomal Protein L10; C25H3.9; ca repeat polymorphism; CD120B; DIS434; T08G11.1; TBP11; TNF Binding Protein 2; TNF R2; TNFR; TNFR2; Tumor Necrosis Factor Receptor 2.
 SOURCE
 Homo sapiens.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (01-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, UK.
 Direct Submission
 Submitted (01-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, UK.
 Requesters: humquery@sanger.ac.uk
 On Dec 2, 1998 this sequence version replaced gi:3724207.

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.
 This sequence is the entire insert of clone 118D24. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>
 118D24 is from the library RPi5 constructed at the Roswell Park Cancer Institute by the group of Peter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:pcyfac2>.

FEATURES

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Query Match 98.5%: Score 2575; DB 9; Length 115602;
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OY	2160	ACAAGGCTTTTCCACCCCTGGATTCAGAGATGTGACACTGGCTGCTCAGTACGCTCAC	AL355998	122105 bp	DNA	linear	HTG 07-SEP-2001					
Db	102841	ACAAAGCTTTTCCACCCCTGGATTCAGAGATGTGACACTGGCTGCTCAGTACGCTCAC	AL355998	Homo sapiens chromosome 1 clone RP5-1125M11, *** SEQUENCING IN	PROGRESS ***	In ordered pieces.						
OY	2220	TGTACACAGAGAGCTGAGGAGAGATCATCTGGAGCCACAGAGTTTGAGGCTGACGAGC	AL355998	9 GI:15523662	HTG: HTGS_PHASE2; HTGS_CANCELLED.	human.	Homo sapiens					
Db	102781	TGTACACAGAGAGCTGAGGAGAGATCATCTGGAGCCACAGAGTTTGAGGCTGACGAGC	AL355998	HTG: HTGS_PHASE2; HTGS_CANCELLED.	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OY	2280	TATGATCGGCCACTACACTCCAGCCTGAGCAACAGAGTGAACCCCTGTCTTTAAAGAA	AL355998	122105 bp	DNA	linear	HTG 07-SEP-2001					
Db	102721	TATGATCGGCCACTACACTCCAGCCTGAGCAACAGAGTGAACCCCTGTCTTTAAAGAA	AL355998	Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk	On Sep 7, 2001 this sequence version replaced gi:13857067.							
OY	2340	AAAAAAGCAGACACGTCTGGAGTCTGGCCAGTTTCTGCCACATTGAGACCCACATAGCA	AL355998	9 GI:15523662	HTG: HTGS_PHASE2; HTGS_CANCELLED.	human.	Homo sapiens					
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OY	2400	CATGATGAGGCGACCTGCCCCCTGGTGACAGTCTCTGGAGAACCTCAGGCTCTCTTG	AL355998	122105 bp	DNA	linear	HTG 07-SEP-2001					
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OY	2460	CATCAGAGGCGACGACCGGGAAAGCATGATTTTGGAGACTCTGTGGGGCTTTGGTCCCT	AL355998	9 GI:15523662	HTG: HTGS_PHASE2; HTGS_CANCELLED.	human.	Homo sapiens					
Db	102541	CATCAGAGGCGACGACCGGGAAAGCATGATTTTGGAGACTCTGTGGGGCTTTGGTCCCT	AL355998	Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk	On Sep 7, 2001 this sequence version replaced gi:13857067.							
OY	2520	TCTGTGTGTGTATATCCACAGACAATTAAGTTTGACCTGTATGCTGTGAGGCAATTC	AL355998	122105 bp	DNA	linear	HTG 07-SEP-2001					
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* NOTE: This is a 'working draft' sequence.

[illegible]

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AUTHORS	Bliren,B., Linton,L., Nusbaum,C. and Lander,E.			
TITLE	Unpublished			
JOURNAL	2 (bases 1 to 187877)			
REFERENCE	Anderson,S., Baldwin,L., Barua,N., Beckert,R., Bede,F., Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P., Dattalano,K., Dewar,K., Domingo,M., Doyle,M., Fennestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galbraith,I.,			

TITLE
JOURNRL
REFERENCE
AUTHORS

Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczek,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McNeters,R., Melrim,J., Menus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivat,T.M., Peterson,K.,
Pierre,N., Pisanil,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thoman,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

Direct Submission
Submitted (10-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 187877)

Anderson,S., Baldwin,J., Baran,C., Lander,E., Abraham,H., Allen,N.,
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Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thoman,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE
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COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7139786.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L6342

Center clone name: 353.D.18

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 177330 bases at least Q40
Consensus quality: 182502 bases at least Q30
Consensus quality: 184382 bases at least Q20
Insert size: 18800; agarose-fp
Insert size: 185477; sum-of-ctrls
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-ctrls

* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1587: contig of 1587 bp in length
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DEFINITION	Sequence 4214 from Patent WO0194629.						

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ORGANISM	Homo sapiens	
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AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppel, D.R. and Weaver, Z.	
TITLE	Cancer gene determination and therapeutic screening using signature gene sets	
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Query Match Best Local Similarity 99.4%: Pred. No. 0: Matches 2502: Conservative 0: Mismatches 15: Indels 0: Gaps 0:

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REFERENCE
1 Schreiber,S., Hampe,J. and Mascheretti,S.
AUTHORS Diagnostic use of polymorphisms in the gene coding for the tnfr
TITLE receptor II and method for detecting non-responders to anti-tnfr
therapy
JOURNAL Patent: EP 1172444-A 49 16-JAN-2002;
FEATURES Research Institute GmbH (DE)
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REFERENCE
1 Schreiber, S., Hampe, J. and Mascheretti, S.
TITLE Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnfr
therapy
JOURNAL Patent: EP 1172444-A 51 16-JAN-2002;
FEATURES
source Conaris Research Institute GmbH (DE)
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QY 817 CAGCATCTCTTCTGAGAGGGGCTTCTGGAGAGAGGATGCTGCTGAGTACCCAT 876
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Db 1947 GAAGACAGAGCAGTCTTCAAGCTGAGGCTGAGATGCGGAGATGGTCTGGGGCTCTGTG 2006
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Best Local Similarly 99.4%: Pred. No. 0;
Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Oy  217  CAACCCAGCTTCACAAATGGAGACACAGATTCCAGCCCTTGGAGTCTCCCGAAGACAGAG 276
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Oy  877  GAAGACAGGACAGTGTCTTACGCTGAGGCTGAGACTGCGGGATGTCTTGGGCTCTGTG 936
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Db  1947 GAAGACAGGACAGTGTCTTACGCTGAGGCTGAGACTGCGGGATGTCTTGGGCTCTGTG 2006

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DEFINITION	Human tumor necrosis factor receptor mRNA, complete cds.	linear	PRI 07-JAN-1995
ACCESSION	M32315		
VERSION	M32315.1	GI:189185	
KEYWORDS	c-myc proto-oncogene; necrosis factor receptor.		
SOURCE	Homo sapiens Lung CDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P., Jerzy,R., Dower,S.R., Cosman,D. and Goodwin,R.G.		
TITLE	A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins		
JOURNAL	Science 248 (1995), 1019-1023 (1990)		
MEDLINE	90260639		
PUBMED	2160731		
COMMENT	Draft entry and computer-readable sequence for [1] kindly submitted by C.A.Smith, 30-MAR-1990, for release after publication.		
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BASE COUNT    781 a 1098 c 1086 g 718 t
ORIGIN

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QY 157	AATTGCACCTGCACATCGTGAACGCTGTATACAGCTTGACACACAGCTCAGTGCCTCC	216			
Db 1227	AATTGCACCTGCACATCGTGAACGCTGTATACAGCTTGACACACAGCTCAGTGCCTCC	1286			
QY 217	CAAGCCAGCTCCACAAATGGGAGACAGATTTCACAGCCCTCGGATCCCGAAGAGAG	276			
Db 1287	CAAGCCAGCTCCACAAATGGGAGACAGATTTCACAGCCCTCGGATCCCGAAGAGAG	1346			
QY 277	CAGGTCCCTCTTCCACAGAGAGATGTGCTTTGGTGCACAGCTTGAGACCCAGAGACC	336			
Db 1347	CAGGTCCCTCTTCCACAGAGAGATGTGCTTTGGTGCACAGCTTGAGACCCAGAGACC	1406			
QY 337	CTGCTGGGGAGCACCCAGAGAAAGCCCGCCCTTGGAGATGCTGATGCTGGATTAAG	396			
Db 1407	CTGCTGGGGAGCACCCAGAGAAAGCCCGCCCTTGGAGATGCTGATGCTGGATTAAG	1466			
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Db 1467	CCCACTTAACCAAGGCGGT	1526			
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Db 1527	ATGACCCCTGGAGAGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1586			
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RESULT 10
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 DEFINITION
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 KEYWORDS
 SOURCE
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 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3492)
 Dembic, Z., Loetscher, H., Gubler, U., Pan, Y. C., Lahm, H. W., Gentz, R.,
 Brockhaus, M. and Lesslauer, W.
 Two human TNF receptors have similar extracellular, but distinct
 intracellular, domain sequences
 Cytokine 2 (4), 231-237 (1990)
 91370690
 196549
 GenBank staff at the National Library of Medicine created this
 entry [NCBI gidsbq 63368] from the original journal article.
 This sequence comes from Figure 1.
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FEATURES
 source
 CDS

Db 2947 AATTTGTTAATTAATTCACCTGAGCTTGAGCTTGGCAGCTGAACATTTGGAGCTGGAG 3006
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Qy 2316 ACTGAGACCTCTCTCTTAAGAAAAAAGTACAGCTGCTGGAGTGGCAGGTTCT 2375
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ACCESSION G26865
VERSION G26865.1 GI:1375115
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 3380)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1995)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CCCACCACTAGACTGCA
Primer B: CACAGAGTCAGGACTTC
STS size: 201
PCR Profile:

Initial Incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM

Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3
Prepared with primer pairs provided by Sandoz, derived from M32315
-- Washington University/Merck EST sequence.
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 2199; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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Qy 217 CAAGCCAGCTCCCAATGGAGACACAGATTTCCAGCCCTCGAGTCCCGAAGACGAG 276
Db 1287 CAAGCCAGCTCCCAATGGAGACACAGATTTCCAGCCCTCGAGTCCCGAAGACGAG 1346
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Db 1347 CAGGTCCCTTCTTCGAAGAGAGATGTCCTTGGTTCACAGCTGAGACCCAGAGACC 1406
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Db 1407 CTGCTGGGGAGCACCGAAGAGAGCCCTGCTGAGTGCCTGATGCTGGATGAAG 1466
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Db 1467 CCCAGTTAACAGAGCCGGTGTGGCTGTGCTAGCCAAAGTGGGCTGAGCCCTGGCAGG 1526
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Db 1527 ATGACCTGCGAAGGGAGCCCTGCTGCTTCAGAGCCGCCCACTAGAGCTGAGAGCTCT 1586
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Db 1587 TTCTGGGCGCAAGTCTCTTAGTGCCTCCACAGCCGACCTCTGACCTGAGAGCC 1646
Qy 577 AAGAGCAGAGGAGAGAGTGGGAAAGCTCTGCTGCCATGCTGTGCTCTTCGGAAG 636
Db 1647 AAGAGCAGAGGAGAGAGTGGGAAAGCTCTGCTGCCATGCTGTGCTCTTCGGAAG 1706
Qy 637 GCTGCTGGGCGATGAGAGTTCGGGGCATGCGGGCAAGTCCCTGACCTCTGAGACTG 696
Db 1707 GCTGCTGGGCGATGAGAGTTCGGGGCATGCGGGCAAGTCCCTGACCTCTGAGACTG 1766
Qy 697 CCCGCGCCAGCTGACACCTGCGACAGCTGCTGTGAGAGCCCTTGGGTTTGTGTTG 756
Db 1767 CCCGCGCCAGCTGACACCTGCGACAGCTGCTGTGAGAGCCCTTGGGTTTGTGTTG 1826
Qy 757 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 816
Db 1827 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1886

Qy	817	GACATCTCTTTCTGACAGGGGCTTCTGAGAGAGGAGTGTGCTGAGTACACCAT	876
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Qy	877	GAGACAGAGCAGTGTCTGAGCTTGAGGCTGAGACTGCGGGATGTCTTGGGGCTTGAG	936
Db	1947	GAGACAGAGCAGTGTCTGAGCTTGAGGCTGAGACTGCGGGATGTCTTGGGGCTTGAG	2006
Qy	937	TAGCAGAGGTGGCAGCCCTGTAGGGAAACGGGGTCTTCAGTTAGCTTACAGAGGCTTG	996
Db	2007	TAGGAGAGGTGGCAGCCCTGTAGGGAAACGGGGTCTTCAGTTAGCTTACAGAGGCTTG	2066
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Qy	1057	GCTGAGGGCGGTGTACCTCAGCTGAGGTTAGAGTTGCGAGACACGCTGGCCAACTGTAA	1111
Db	2127	GCTGAGGGCGGTGTACCTCAGCTGAGGTTAGAGTTGCGAGACACGCTGGCCAACTGTAA	2186
Qy	1117	AACCCATCTCTACTATAAATATACAGAAATTAAGCCGGCGTGTGGCGGCGACCTATAGTC	1176
Db	2187	AACCCATCTCTACTATAAATATACAGAAATTAAGCCGGCGTGTGGCGGCGACCTATAGTC	2246
Qy	1177	CCAGCTACTCAGAAACCTGAGGCTGGGAAATCGTTTAAACCGGGGAAAGGGAGGTTGGAG	1236
Db	2247	CCAGCTACTCAGAAACCTGAGGCTGGGAAATCGTTTAAACCGGGGAAAGGGAGGTTGGAG	2306
Qy	1237	GGAGCCGAGATCACGCCACTGCACATCCAGCCTGGGCGACAGACGAGAGTCTGTCTCAA	1296
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Qy	1297	AGAAAAAAGAAAAAGCAGCGGCTCCAAATGCTAACTGTGCTTTGTACCATGTGTGAA	1356
Db	2367	AGAAAAAAGAAAAAGCAGCGGCTCCAAATGCTAACTGTGCTTTGTACCATGTGTGAA	2426
Qy	1357	ACTCAGATGCCCAGAGGGGCCAGGACGCCACCATATTCAGTGTCTGTGGCTGGGCAAGA	1418
Db	2427	ACTCAGATGCCCAGAGGGGCCAGGACGCCACCATATTCAGTGTCTGTGGCTGGGCAAGA	2486
Qy	1417	TAGCCACTTCTAACTAGAAATCTGGCCAAATTTTAAAAAAGTAGTACCCTACAGGCCA	1476
Db	2487	TAGCCACTTCTAACTAGAAATCTGGCCAAATTTTAAAAAAGTAGTACCCTACAGGCCA	2546
Qy	1477	ACAAGCCAACAGACAAGCCAAACCTGTGCCAGCCACATCCAACCCCCACACTGCCATTTGC	1536
Db	2547	ACAAGCCAACAGACAAGCCAAACCTGTGCCAGCCACATCCAACCCCCACACTGCCATTTGC	2606
Qy	1537	ACCCTCGGCTTCACTCCGGTGTGTGCTGCAAGCCCGCGGCTCTTCCTTGTGTCCTAGG	1596
Db	2607	ACCCTCGGCTTCACTCCGGTGTGTGCTGCAAGCCCGCGGCTCTTCCTTGTGTCCTAGG	2666
Qy	1597	CCACACATCTCTCTTTCAGGGAATTTTCAGGAATCTAGATGTAGTGAAGCTCTGTAGCCAT	1656
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Qy	1657	CTCTCTACTCTTACCTCAGCCTAGACCTCTCTCCAGAGAGGGTGGGTTCTCTCTTC	1716
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Qy	1717	CCCACTCCCACTTCAATTCCTGAGGAGCCCAAAAGGGGCTGCTCCCACTTTGGTACATG	1776
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	2967	CCCAATTGAGTGCAGCCTTCCCTCCAGAGGCCAGGGCCCTGCAGAGGGGAAACCACTGT	3026
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	3027	AGCCTTCCCGGATTTCTGGGAGGAAGAGGTGTGGGGGCTCTGGAAAGGCTCAGTCTCA	3086
QY	2017	GGAGCATGGGGATTAAGAGAGAGGCATGAATTGTCTACGACAGACAGGGCAGCGTGATA	2076
	3087	GGAGCATGGGGATTAAGAGAGAGGCATGAATTGTCTACGACAGACAGGGCAGCGTGATA	3146
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	3147	AATTGTTGATAAATTCCTCAGTGCAGCTTGAGCTTGGCAGCTAACTATTGGAGGCTGGAGA	3206
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	3207	GCCCGAGCCATTACCATGGAGACAAAGAGGGTTTCCACCTGGAAATCAAGATGTCAGACT	3266
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	3267	GGCTGGCTGCAGTGCAGCTGCACCTGTACTAGAGAGCCTGAGGGAGGAGTCACTGGAGCC	3326
QY	2257	AGGAGTTTGAGGCTGCAGCAGCATGATGATGGCCCACTACATCCAGCCCTGAGC	2310
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Query Match			
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Pred. No. 0			
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Gaps 2			
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Oy 149 CCCAGGTAAATGTGTCATCGTGAACGTCGTAGCAGCTTGACCACAGCTCACAGT 208

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Dh 1222 CTGGCAGATACCTCTGGGAAAGGGCCCTGCTTCCAGGCCCCCACCACCTAGAGCTCT 1281

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Dh 2301 CCATTTCACACCTCCGCTTCACTCCGCTGCTGCTCAG 2339

RESULT 13

HUMTNFR11 2394 bp mRNA linear PRI 03-SEP-1994

LOCUS Human tumor necrosis factor receptor II (TNFR11) mRNA, complete

DEFINITION

cds.

Accession M55994.1 GI:339757

Version M55994.1 GI:339757

Keywords glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.

Source Human histiocytic lymphoma cell line U937, cDNA to mRNA.

Organism Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 2394)

Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W.,

Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.

A second tumor necrosis factor receptor gene product can shed a

naturally occurring tumor necrosis factor inhibitor

Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)

91045991

2172983

Location/Qualifiers

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93..1478

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1542

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2001


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Db 1170 GAGGCCCGGGCCAGCACCGGAGCTCAGATTCTTCCCTGGTGCCATGGAGCCAGCTC 1229
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QY 277 CAGGTCCCTTCTCCAGAGAGGAATGTGCTTGGTCCACAGCTGAGAGAGCCAGAGACC 336
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VERSION A78517.1 GI:6090179
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AUTHORS Mett, I. and Wallach, D.
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Search completed: December 6, 2002, 03:47:59
Job time : 6720.27 secs

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DR	WPI: 2000-412362/35.		
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PT	Identifying individuals at risk of developing osteoporosis comprises		
PT	assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene		
XX	in a DNA sample from an individual -		
PS	Claim 2; Page 17-18; 21pp; English.		
XX			
CC	The present sequence comprises exon 10 of the human tumour necrosis		
CC	factor alpha receptor 2 (TNFR2) gene. The sequence contains three		
CC	polymorphic sites. By determining the genotype of an individual it is		
CC	possible to identify those at risk of osteoporosis, which is		
CC	characterised by low bone density and fragile bones, later in life. Those		
CC	at greatest risk are those who possess allele 1, which is the rarest		
CC	allele. This is particularly useful as many cases of osteoporosis go		
XX	undetected at present.		
XX			
SO	Sequence 2613 BP: 553 A; 750 C; 742 G; 568 T; 0 other;		
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DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:4214.
XX
KM Human: cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KM Stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KM Cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KM gene; ds.
XX
OS Homo sapiens.
XX
PN W0200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 18-SEP-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234034P.
PR 22-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.

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PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.

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(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S:
 Soppet DR, Weaver Z;
 WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a
 chemical agent to be tested for anti-neoplastic activity, and
 determining a change in expression of a gene of a signature gene set -

Claim 1; SEQ ID 4214; 44pp: English.

The present invention describes a method (M1) for screening for an
 anti-neoplastic agent. The method involves exposing cells to a chemical
 agent to be tested for anti-neoplastic activity, determining a change in
 expression of at least one gene (1) of a signature gene set, where (1)
 comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 expression is indicative of anti-neoplastic activity. (1) has cytosolic
 activity and can be used in gene therapy. M1 can be used for screening
 an anti-neoplastic agent, and can be used for producing a product which
 is the data collected with respect to the anti-neoplastic agent as a
 result of M1, and the data is sufficient to convey the chemical
 structure and/or properties of the agent. M1 can be used in the
 treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms tumour.

Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other:

Query Match 95.48; Score 2493; DB 24; Length 3683;

Best Local Similarity 99.48; Pred. No. 0;

Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy 97 GACCCCAACCCATCTGTTGTTGAGATGTTCCCTGGTGGCCATGAGGACCCAGCTC 156
Db 1167 GAGGCCCGGCGCAGCACCAGGAGCTCAAGATTCTTCCCTGGTGGCCATGAGGACCCAGCTC 1226
Qy 157 AATGTACCTTCATCGTGAACGCTGTAGAGCTGTGACCAACAGCTACAGTCTCTCC 216
Db 1227 AATGTACCTTCATCGTGAACGCTGTAGAGCTGTGACCAACAGCTACAGTCTCTCC 1286
Qy 217 CAAGCCAGCTTCACAAATGGGAGACACAGATTCAGCCCTCGGAGTCCCGGAAGACGAG 276
Db 1287 CAAGCCAGCTTCACAAATGGGAGACACAGATTCAGCCCTCGGAGTCCCGGAAGACGAG 1346

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OY	277	CATCCCCCTTCTCCAGGAGGAATGTGCTTTCGGTCCACAGCTGAGACGCCACAGACC	336
Db	1347	CAGGTCCCCCTTCTCAAGGAGGAATGTGCTTTCGGTCCACAGCTGAGACGCCACAGACC	1408
OY	337	CTGTGGGGAGCACCGAAGAAGACCCCTCCCTTGGAGTGCCTGATCTCTGGATTGAG	396
Db	1407	CTGTGGGGAGCACCGAAGAAGACCCCTCCCTTGGAGTGCCTGATCTCTGGATTGAG	1466
OY	397	CCCACTTAACAGGCCCGGTGGGCTGTGCTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG	456
Db	1467	CCCACTTAACAGGCCCGGTGGGCTGTGCTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG	1526
OY	457	ATGACCCCTGGCAAGGGGCCCTTGGTCCCTTCAGGCCCCCACACTAGACTGTGAGGCTCT	516
Db	1527	ATGACCCCTGGCAAGGGGCCCTTGGTCCCTTCAGGCCCCCACACTAGACTGTGAGGCTCT	1586
OY	517	TTCTGGGCCAAGTTCCTGTAGTGCCTTCACAGCCGACGCCCTGTGACCTGACGAGCC	576
Db	1587	TTCTGGGCCAAGTTCCTGTAGTGCCTTCACAGCCGACGCCCTGTGACCTGACGAGCC	1648
OY	577	AAGAGCAGAGGCACCGAGTGGGGAAAAAGCCTGTGCTGCATGTGTGTGCCCTCTGGAG	636
Db	1647	AAGAGCAGAGGCACCGAGTGGGGAAAAAGCCTGTGCTGCATGTGTGTGCCCTCTGGAG	1706
OY	637	GCTGCTGGGCATGGAGCTTCGGGGCATGCTGGGGCAAGTCCCTGACTCTGTGACCTG	696
Db	1707	GCTGCTGGGCATGGAGCTTCGGGGCATGCTGGGGCAAGTCCCTGACTCTGTGACCTG	1766
OY	697	CCCCGCCCAGCTGCACCTGCCACCTGTGCTTGAGACCCCTTGGCTTTTGTGTGTG	756
Db	1767	CCCCGCCCAGCTGCACCTGCCACCTGTGCTTGAGACCCCTTGGCTTTTGTGTGTG	1826
OY	757	TTTGTGTGTGTGTGTGTGTTCGCCCTGGGCTGTGCCAGCTGTGACTCCGAAAAACC	816
Db	1827	TTTGTGTGTGTGTGTGTGTTCGCCCTGGGCTGTGCCAGCTGTGACTCCGAAAAACC	1886
OY	817	CAGCATCTTTTCTGCAGAGGGCTTCTGTGAGAGGAGGGATGTGCTGAOTCACCAT	876
Db	1887	CAGCATCTTTTCTGCAGAGGGCTTCTGTGAGAGGAGGGATGTGCTGAOTCACCAT	1946
OY	877	GAACACAGGACAGTGCCTTCAGGCGTGAGAGCTGCGGGATGTGCTCGGGGCTGTG	936
Db	1947	GAACACAGGACAGTGCCTTCAGGCGTGAGAGCTGCGGGATGTGCTCGGGGCTGTG	2006
OY	937	TAGGAGGAGGTGGCAGGCCCTGTAGGGAACGGGGTCTCTCAAGTTAGCTCAGAGAGCTTG	996
Db	2007	TAGGAGGAGGTGGCAGGCCCTGTAGGGAACGGGGTCTCTCAAGTTAGCTCAGAGAGCTTG	2066
OY	997	GAAGCATTCACCTCAGGCCAGGTGCAGTGGCTCAGGCTATGATCCAGCACATTTGGGAG	1056
Db	2067	GAAGCATTCACCTCAGGCCAGGTGCAGTGGCTCAGGCTATGATCCAGCACATTTGGGAG	2126
OY	1057	GCTGAGCGGGGTGATACCTGTAGGTTAGAGTGGAGACAGCTGGCCAAATGGTAA	1116
Db	2127	GCTGAGCGGGGTGATACCTGTAGGTTAGAGTGGAGACAGCTGGCCAAATGGTAA	2186
OY	1117	AACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGCTGTGGCGGGCACCTATAGTC	1176
Db	2187	AACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGCTGTGGCGGGCACCTATAGTC	2246
OY	1177	CCACCTCTCAGAAAGCTAGGCTGGGAAATGTTGAAACCCGGGACCGGAGGTTGCAG	1236
Db	2247	CCACCTCTCAGAAAGCTAGGCTGGGAAATGTTGAAACCCGGGACCGGAGGTTGCAG	2306
OY	1237	GGAGCCGAGATCAAGCCACTGCACCTCCACGCTGGGGCAGACAGACGAGAGTGTCTCAA	1296
Db	2307	GGAGCCGAGATCAAGCCACTGCACCTCCACGCTGGGGCAGACAGACGAGAGTGTCTCAA	2366
OY	1297	AGAAAAAAGAACGAGCCGCTCCAAATGTCTAAGTTGCTTTTGTACATGGTGTGAA	1356
Db	2367	AGAAAAAAGAACGAGCCGCTCCAAATGTCTAAGTTGCTTTTGTACATGGTGTGAA	2426

QY	1357	AGCAGATGCCCGAGAGGGGCCCGACGGCCACCACCATATTTGAGTGTGTGGCTTGCGGCAMAGA	1416
Db	2427	AGTCAGATGCTCCGAGAGGGCCGACGGCCACACCATATTCAGTGTGTGGCTTGCGGCAGAGA	2486
QY	1417	TAAAGCACTTCTAACTAGAGAAATGTGGCAATTTTTTAAAAAGTAAGTATCACTCAGGCCA	1476
Db	2487	TAAAGCACTTCTAACTAGAGAAATGTGGCAATTTTTTAAAAAGTAAGTATCACTCAGGCCA	2546
QY	1477	ACAAGCGAAGCAAAAGCCAAACTGTGCCAGCCAGCATCCCAACCCCCACCTGCATTTTGC	1536
Db	2547	ACAAGCGAAGCAAAAGCCAAACTGTGCCAGCCAGCATCCCAACCCCCACCTGCATTTTGC	2606
QY	1537	ACCCTTCGGCTTACATCCCGTGTGGCTGGAGCCCGCGCTCTCTTCCTTGTGCTGTCTAGG	1596
Db	2607	ACCCTTCGGCTTACATCCCGTGTGGCTGGAGCCCGCGCTCTCTTCCTTGTGCTGTCTAGG	2666
QY	1597	CCACACCAATCTCTCTTCAGGGAATTTTCAGGAACCTAGAGATGACTAGTCTCTGTAGCCAT	1656
Db	2667	CCACACCAATCTCTCTTCAGGGAATTTTCAGGAACCTAGAGATGACTAGTCTCTGTAGCCAT	2726
QY	1657	CTCTCTACTCTGACCTGACCCGATAGACCCCTGCTCTCCGCCCAAGGGGTGGTTCCTTTC	1716
Db	2727	CTCTCTACTCTGACCTGACCCGATAGACCCCTGCTCTCCGCCCAAGGGGTGGTTCCTTTC	2786
QY	1717	CCCACTCCCACTTCAATTTCTTGCGGCCCAACAGGGGTGCTCCCTGCACATTTGTGTACATG	1776
Db	2787	CCCACTCCCACTTCAATTTCTTGCGGCCCAACAGGGGTGCTCCCTGCACATTTGTGTACATG	2846
QY	1777	GGCAGTGTGATCCCAAGTGTCCAGCTCTTGTGTGTGCTGTGTGCTGTGCTGTGGCTGTG	1836
Db	2847	GGCAGTGTGATCCCAAGTGTCCAGCTCTTGTGTGTGCTGTGTGCTGTGCTGTGGCTGTG	2906
QY	1837	TGTAGCAAGTGTGGTAAATGTTAAATGGCTGCTTGAAGGCCATGACCTGGAGATTCCMC	1896
Db	2907	TGTAGCAAGTGTGGTAAATGTTAAATGGCTGCTTGAAGGCCATGACCTGGAGATTCCMC	2966
QY	1897	CCCATTAGAGTACGCTTCCCTCCCTCCACAGGGCGCCCTGACAGAGGGGAAACCAGTGT	1956
Db	2967	CCCATTAGAGTACGCTTCCCTCCCTCCACAGGGCGCCCTGACAGAGGGGAAACCAGTGT	3026
QY	1957	ACCTTTGCCCGGATTTCTGGAGGAAGCAGGTTGAGGGGCTCTGTGAAGGGCTCACTCTCA	2016
Db	3027	ACCTTTGCCCGGATTTCTGGAGGAAGCAGGTTGAGGGGCTCTGTGAAGGGCTCACTCTCA	3086
QY	2017	GGAGCATGGGGTAAAGGAGAAAGCCATGAATTTGTCTAGCAGAGCAGGGGCGAGGCTGATA	2076
Db	3087	GGAGCATGGGGTAAAGGAGAAAGCCATGAATTTGTCTAGCAGAGCAGGGGCGAGGCTGATA	3146
QY	2077	AATTTGTAATAATTCACACTGGACTTGGAGCTTGGAGCTGAACTATTGGAGGGTGGAGA	2136
Db	3147	AATTTGTAATAATTCACACTGGACTTGGAGCTTGGAGCTGAACTATTGGAGGGTGGAGA	3206
QY	2137	GGCCAGCCATTACATGTGAGAACAAAGAGGTTTTCCACCTGGGAATCAAGATGTGACACT	2196
Db	3207	GGCCAGCCATTACATGTGAGAACAAAGAGGTTTTCCACCTGGGAATCAAGATGTGACACT	3266
QY	2197	GGCTTGGCTGCACTGACGTGCACTTACTCAGAGAGCTGTAGGGGAGATCACTGGAGCCC	2256
Db	3267	GGCTTGGCTGCACTGACGTGCACTTACTCAGAGAGCTGTAGGGGAGATCACTGGAGCCC	3326
QY	2257	AGGATTTTGAGGCTGACAGCAAGCTTGAATGCGGGCCACTACACTCCAGGCTGAGCAACGA	2316
Db	3327	AGGATTTTGAGGCTGACAGCAAGCTTGAATGCGGGCCACTACACTCCAGGCTGAGCAACGA	3386
QY	2317	GTGAGACCTGTCTTTAAAGAAAAAAAAGTCAAGACTGTGGGACTGTGGCCAGGTTTTCTG	2376
Db	3387	GTGAGACCTGTCTTTAAAGAAAAAAAAGTCAAGACTGTGGGACTGTGGCCAGGTTTTCTG	3446
QY	2377	CCCAATTGGAGCCCAATGAGGAATGATGTGAGGCCACACTGCCCCCTGTGTGGAACATGCTCT	2436
Db	3447	CCCAATTGGAGCCCAATGAGGAATGATGTGAGGCCACACTGCCCCCTGTGTGGAACATGCTCT	3506
QY	2437	GGGAGAACCTGAGGCTTCTTTGGCATGCAAGGGGAGACCCGGGAAGCATGAATTTTGAG	2496


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DB 3507 GGGAGAACCTCAGGCTTCTTGGCATCAGAGCGACCGCGAAGCATATTTGGAG 3566
QY 2497 ACTCTGTGGGGCTTGTTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 2556
DB 3567 ACTCTGTGGGGCTTGTTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 3626
QY 2557 CACTGTATCTGAGAGCGCATCTCTTATCAATAAACCTGTTTGTAAAAAAA 2613
DB 3627 CACTGTATCTGAGAGCGCATCTCTTATCAATAAACCTGTTTGTAAAAAAA 3683

RESULT 4
ABK33465
ID ABK33465 standard; DNA; 3683 BP.
AC ABK33465;
XX
XX
XX 23-APR-2002 (first entry)
DE Human TNF receptor II gene.
XX
XX Human: anti-tumour necrosis factor receptor II; TNF receptor II;
KW chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW inflammatory disorder; chronic disease; receptor; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 90..1475
XX FT /*tag= a
XX FT /*product= "TNF receptor II"
XX FT sig_peptide 90..135
XX FT /*tag= b
XX FT mat_peptide 156..1472
XX FT /*tag= c
XX
XX EPI172444-A1.
XX
XX 16-JAN-2002.
XX
XX 10-JUL-2000: 2000EP-0114786.
XX
XX 10-JUL-2000: 2000EP-0114786.
XX
XX (COMA-) COMARIS RES INST GMBH.
XX
XX Schreiber S, Hampe J, Mascheretti S;
XX
XX WPI: 2002-156651/21.
XX
XX P-PSDB: AAU75172.
XX
XX Detecting non-responders to anti-human necrosis factor therapy,
XX comprises testing an individual for homozygosity for a single
XX nucleotide polymorphism in the gene coding for the tumour necrosis
XX factor receptor II.
XX
XX Disclosure: Page 23-27; 45pp: English.
XX
XX The present invention relates to a method for detecting non-responders
XX to anti-tumour necrosis factor (TNF) therapy. The method involves testing
XX an individual for homozygosity for at least one single nucleotide
XX polymorphism (SNP) in the gene coding for TNF receptor II, which is
XX located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
XX A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
XX Met156Arg respectively, are also described. The method of the invention
XX is useful for detecting non-responders to anti-TNF therapy such as
XX infliximab therapy, or therapy of Crohn's disease. The genes containing
XX the 2 novel polymorphisms are useful for diagnostic purposes in
XX inflammatory, malignant or other chronic diseases. The present sequence
XX encodes for human TNF receptor II.
XX
XX Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

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Query Match 95.4%; Score 2493; DB 24; Length 3683;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 97 GACCCCAACCCCATCTTGTGCTTACAGATTCCTCCCTGTGGCCATGGACCCAGTGC 156
DB 1167 GAGGCCCGGGCCAGCAGCCGGGAGCTCAGATTCCTCCCTGTGGCCATGGACCCAGTGC 1226
QY 157 AATGTACCTGCATGCTAGAGCTGTGTAGAGCTGTGACACAGCTACAGTGTCTCC 216
DB 1227 AATGTACCTGCATGCTAGAGCTGTGTAGAGCTGTGACACAGCTACAGTGTCTCC 1286
QY 217 CAAGCCACCTCCACAAATGGAGACACAGATTCAGACCCCTGGAGTCCCGAAGAGAG 276
DB 1287 CAAGCCACCTCCACAAATGGAGACACAGATTCAGACCCCTGGAGTCCCGAAGAGAG 1346
QY 277 CAGGTCCCTCTCCAGAGGAATGTGCTTTCGGTACAGCTGAGAGCCAGAGACC 336
DB 1347 CAGGTCCCTCTCCAGAGGAATGTGCTTTCGGTACAGCTGAGAGCCAGAGACC 1406
QY 337 CTGCTGGGAGACACCGAAGAGACCCCTGCTTGTAGTGGCTGATGCTGGATGAAG 396
DB 1407 CTGCTGGGAGACACCGAAGAGACCCCTGCTTGTAGTGGCTGATGCTGGATGAAG 1466
QY 397 CCCAGTTAACCAAGCCGGTGTGGCTGTGCTAGCCAAAGTGGGCTGAGCCCTGGCAG 456
DB 1467 CCCAGTTAACCAAGCCGGTGTGGCTGTGCTAGCCAAAGTGGGCTGAGCCCTGGCAG 1526
QY 457 ATGACCCCTGCAAGGGGCGCTGCTTCCAGGCGCCCGACCACTAGAGACTGTAGGCTCT 516
DB 1527 ATGACCCCTGCAAGGGGCGCTGCTTCCAGGCGCCCGACCACTAGAGACTGTAGGCTCT 1586
QY 517 TTCTGGGCAAGTCTCTAGTGCCTTCACAGCCGACGCTCCCTGACCTGACGAGCC 576
DB 1587 TTCTGGGCAAGTCTCTAGTGCCTTCACAGCCGACGCTCCCTGACCTGACGAGCC 1646
QY 577 AAGAGCAGAGGACGAGTGGGGAAGCCCTGTGCTGCCATGCTGTGCTTCCGGAAG 636
DB 1647 AAGAGCAGAGGACGAGTGGGGAAGCCCTGTGCTGCCATGCTGTGCTTCCGGAAG 1706
QY 637 GCTGGCTGGGATGAGCTTCGGGGCATGCTGGGGCAATCCCTGACCTCTGTACCTG 696
DB 1707 GCTGGCTGGGATGAGCTTCGGGGCATGCTGGGGCAATCCCTGACCTCTGTACCTG 1766
QY 697 CCCGCCACAGCTGACCTGCGACGCTTGTGAGGACCTTGGGTTTGTGTTTG 756
DB 1767 CCCGCCACAGCTGACCTGCGACGCTTGTGAGGACCTTGGGTTTGTGTTTG 1826
QY 757 TTTGTTGTTGTTGTTTCTCCCTGGGCTTGTGCGCTGTGCTTCCAGAAACC 816
DB 1827 TTTGTTGTTGTTGTTTCTCCCTGGGCTTGTGCGCTGTGCTTCCAGAAACC 1886
QY 817 CAGCATCTTTTGTGAGAGGGGCTTGTGAGAGAGAGATGTGCGTAGTCAACCAT 876
DB 1887 CAGCATCTTTTGTGAGAGGGGCTTGTGAGAGAGAGATGTGCGTAGTCAACCAT 1946
QY 877 GAAGACAGACACTGCTCTAGAGCTGAGAGCTGCGGATGCTCTGGGGCTGTG 936
DB 1947 GAAGACAGACACTGCTCTAGAGCTGAGAGCTGCGGATGCTCTGGGGCTGTG 2006
QY 937 TAGGAGAGAGTGGCAGCCCTGTAGGGAAGGGGCTTTCAAAGTTAGTCAAGAGGCTTG 996
DB 2007 TAGGAGAGAGTGGCAGCCCTGTAGGGAAGGGGCTTTCAAAGTTAGTCAAGAGGCTTG 2066
QY 997 GAAAGCATCACTCAGGCGAGGTGAGTGGCTACAGCTATGATCCAGCACTTTGGAG 1056
DB 2067 GAAAGCATCACTCAGGCGAGGTGAGTGGCTACAGCTATGATCCAGCACTTTGGAG 2126
QY 1057 GCTGAGCGGGTGAATCACTGAGGTTAGAGGTTGAACACAGCTGGGCCAATGTGTAA 1116
DB 2127 GCTGAGCGGGTGAATCACTGAGGTTAGAGGTTGAACACAGCTGGGCCAATGTGTAA 2186

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OY 1117 AACCCATCTCTACTAAAAATACAGAAATTAGCGGGGCGTGGGGGGGCGGCGACCTATAGTC 1176
    |||||||
DB 2187 AACCCATCTCTACTAAAAATACAGAAATTAGCGGGGCGTGGGGGGGCGGCGACCTATAGTC 2246
OY 1177 CCAGCTACTCAGAGGCTGAGGCTGGGAAATGTTTGAACCCGGGAAAGCGAGGTTGGAG 1236
    |||||||
DB 2247 CCAGCTACTCAGAGGCTGAGGCTGGGAAATGTTTGAACCCGGGAAAGCGAGGTTGGAG 2306
OY 1237 GAGCGCGAGATCAGCGCACTGACATCCAGCCTGGGCGAGAGCGCAGAGCTGTCTCAAA 1296
    |||||||
DB 2307 GAGCGCGAGATCAGCGCACTGACATCCAGCCTGGGCGAGAGCGCAGAGCTGTCTCAAA 2366
OY 1297 AGAAAAAAGACCGCGCTCCAAATGCTAAGTTCCTTTTGTACATGGTGTGAA 1356
    |||||||
DB 2367 AGAAAAAAGACCGCGCTCCAAATGCTAAGTTCCTTTTGTACATGGTGTGAA 2426
OY 1357 AGTCAGATCCCGAGAGGCGCCAGGAGGCGCACCATATTCAGTGTGGCCTGGGCAAGA 1416
    |||||||
DB 2427 AGTCAGATCCCGAGAGGCGCCAGGAGGCGCACCATATTCAGTGTGGCCTGGGCAAGA 2486
OY 1417 TAACGCACTTCTAAGTAAATCTGCCAATTTTAAAAAAGTAGTACCACTCAGGCCA 1476
    |||||||
DB 2487 TAACGCACTTCTAAGTAAATCTGCCAATTTTAAAAAAGTAGTACCACTCAGGCCA 2546
OY 1477 ACAAGCCAGCAAGCAAGCCAAACTCTGCAGGCGACATCCAAACCCCGCAGCTTGTTC 1536
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DB 2547 ACAAGCCAGCAAGCAAGCCAAACTCTGCAGGCGACATCCAAACCCCGCAGCTTGTTC 2606
OY 1537 ACCCTCCGCTTCTACTCCGGGTGTGCTGCAGCGCCGCGCTCTTCTGCTGTCTAGG 1596
    |||||||
DB 2607 ACCCTCCGCTTCTACTCCGGGTGTGCTGCAGCGCCGCGCTCTTCTGCTGTCTAGG 2666
OY 1597 CCACAGCATCTCTTTCAGAGGAATTTTCAGAACTAGAGATGAGTACCTCGTAGCCAT 1656
    |||||||
DB 2667 CCACAGCATCTCTTTCAGAGGAATTTTCAGAACTAGAGATGAGTACCTCGTAGCCAT 2726
OY 1657 CTCTCTACTCTCTACTCAGCCTAGACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTTC 1716
    |||||||
DB 2727 CTCTCTACTCTCTACTCAGCCTAGACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTTC 2786
OY 1717 CCCACTCCCGACCTTCAATTCCTGGGCGCCCAAGAGGGGTGGCGCCACTTGGTACATG 1776
    |||||||
DB 2787 CCCACTCCCGACCTTCAATTCCTGGGCGCCCAAGAGGGGTGGCGCCACTTGGTACATG 2846
OY 1777 GCCAGTGTGATCCCAAGTGGCCAGTGTGTCTGCTGTCTGTGCTGTCTGTGCTGTG 1836
    |||||||
DB 2847 GCCAGTGTGATCCCAAGTGGCCAGTGTGTCTGCTGTCTGTGCTGTGCTGTGCTGTG 2906
OY 1837 TGTAGCCAAAGTGGTGAATGGCTGCTCTGGAAGCCAGAGCTGGGATTCCTC 1896
    |||||||
DB 2907 TGTAGCCAAAGTGGTGAATGGCTGCTCTGGAAGCCAGAGCTGGGATTCCTC 2966
OY 1897 CCCATTAGATCAGCTTCCCGCTCCAGGCGCAGGGCCCTGCGAGAGGGGAAACAGTAGT 1956
    |||||||
DB 2967 CCCATTAGATCAGCTTCCCGCTCCAGGCGCAGGGCCCTGCGAGAGGGGAAACAGTAGT 3026
OY 1957 AGCCTGGCGCGGATTTCTGGGAGGAAGCAGTGTGAGGGCTCTCTGGAAGGCTCAGTCTCA 2016
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DB 3027 AGCCTGGCGCGGATTTCTGGGAGGAAGCAGTGTGAGGGCTCTCTGGAAGGCTCAGTCTCA 3086
OY 2017 GGACCATGGGATTAAGAGAGAGCATGAATTTGCTTAGCAGAGCAGGGCGAGGGTGATA 2076
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DB 3087 GGACCATGGGATTAAGAGAGAGCATGAATTTGCTTAGCAGAGCAGGGCGAGGGTGATA 3146
OY 2077 AATTGTTGATTAATTTCCACTGTGAGCTTGAGCTGCGACCTGAACATATTCGAGGGTGAGAG 2136
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DB 3147 AATTGTTGATTAATTTCCACTGTGAGCTTGAGCTGCGACCTGAACATATTCGAGGGTGAGAG 3206
OY 2137 GCCCAGCATTTACATGGAGAGCAAGAGGGTTTCCACCTCGAATCAGATGTCACT 2196
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DB 3207 GCCCAGCATTTACATGGAGAGCAAGAGGGTTTCCACCTCGAATCAGATGTCACT 3266
OY 2197 GCGTGGCTGAGTAGCAGCTGTACTCAGAGGCTGAGGGAGGATCAGTGAAGCC 2256

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DB 3267 GCGTGGCTGAGTAGTACGTGACCTGACCTGTACTCAGAGAGGCTGAGGGAGGATCAGTGAGACCC 3326
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OY 2267 AGGAGTTGAGGCTGCGACGCGAGCTATGATGCGCCGCTACACTCAGCTGAGCAACAGA 2316
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DB 3327 AGGAGTTGAGGCTGCGACGCGAGCTATGATGCGCGCAGCTACACTCAGCTGAGCAACAGA 3386
OY 2317 GTGAGACCTGCTCTTAAAGAAAAAAGTAGAGATGCTGGGAGCTGGGAGGTTCTG 2376
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DB 3387 GTGAGACCTGCTCTTAAAGAAAAAAGTAGAGATGCTGGGAGCTGGGAGGTTCTG 3446
OY 2377 CCCCATTTGACACCCACATGAGAGATGATGAGCGCACCTGCCCTGGTGGACAGTCTG 2436
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DB 3447 CCCCATTTGACACCCACATGAGAGATGATGAGCGCACCTGCCCTGGTGGAGTCTG 3506
OY 2437 GGGAGACCTCAGGCTTCCCTGGATCAGAGGCGCAGAGCCGGGAAACGATGAATTTGGAG 2496
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DB 3507 GGGAGACCTCAGGCTTCCCTGGATCAGAGGCGCAGAGCCGGGAAACGATGAATTTGGAG 3566
OY 2497 ACTGTGGGGGCTTGGTTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2556
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DB 3567 ACTGTGTGGGGCTTGGTTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3626
OY 2557 CACTGTATGCTGAGACGGCATTCCTGCTTATCAATAAACCTGTTGTTTAAAAAAA 2613
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DB 3627 CACTGTATGCTGAGACGGCATTCCTGCTTATCAATAAACCTGTTGTTTAAAAAAA 3683

RESULT 5
ABK33466
ID ABK33466 standard; DNA: 3683 BP.
XX
AC ABK33466;
XX
DT 23-APR-2002 (first entry)
XX
DE Human TNF receptor II gene with SNP in exon 2.
XX
KW Human: anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW Chromosome 1p36; Infliximab therapy; Crohn's disease; malignant disorder;
KW Inflammatory disorder; Chronic disease; receptor; gene;
KW Single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 90..1475
FT FT /*tag= a
FT sig_peptide /product= "TNF receptor II variant #1"
FT FT /*tag= b
FT mat_peptide 150..1472
FT FT /*tag= c
FT FT replace (257, A)
FT FT /*tag= d
FT FT /standard_name= "Single nucleotide polymorphism"
XX
PN EP1172444-A1.
XX
PD 16-JAN-2002.
XX
PE 10-JUL-2000; 2000EP-0114786.
XX
PF 10-JUL-2000; 2000EP-0114786.
XX
PR 10-JUL-2000; 2000EP-0114786.
XX
PA (CONA-) CONARIS RES INST GMBH.
XX
PI Schreiber S, Hampe J, Mascheretti S;
XX
XX WPI; 2002-156651/21.
XX
XX P-PSDB; AAU75173.
XX
PT Detecting non-responders to anti-human necrosis factor therapy.

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PT comprises testing an individual for homozygosity for a single
PT nucleotide polymorphism in the gene coding for the tumour necrosis
PT factor receptor II

XX Claim 15: Page 29-33; 45pp; English.

XX The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC A/G) and one in exon 6 (position 587 T/G) which result in Lys587Asn and
CC Met168Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC infliximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC represents the human TNF receptor II gene containing the SNP in exon 2.
XX
XX
50 Sequence 3683 BP: 780 A; 1098 C; 1087 G; 718 T; 0 other:

Query Match 95.48; Score 2493; DB 24; Length 3683;
Best Local Similarity 99.48; Pred. No. 0;

Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	97	GACCCCAACCCCATCTTGCTGCTAGACAGATTCTTCCCTGGTGGCCATGGGACCCAGATC	156
DB	1167	GAGCCCGGGGCGACACCGGAGCTCAGATTCTTCCCTGGTGGCCATGGGACCCAGATC	1226
QY	157	AATGTACCTGTCATCTGTAAGAGCTCTGAGACAGCTTGACACAGCTCAGTCTCTCC	216
DB	1227	AATGTACCTGTCATCTGTAAGAGCTCTGAGACAGCTTGACACAGCTCAGTCTCTCC	1286
QY	217	CAACCCAGCTCCAAATGGGAGACAGATTCCAGCCCTCGAGTCCCGGAGGACAG	276
DB	1287	CAACCCAGCTCCAAATGGGAGACAGATTCCAGCCCTCGAGTCCCGGAGGACAG	1346
QY	277	CAGTCCCTTCTTCCAAAGAGAAATGTCTTTCGATCAGCTGAGAGCCAGAGAC	336
DB	1347	CAGTCCCTTCTTCCAAAGAGAAATGTCTTTCGATCAGCTGAGAGCCAGAGAC	1406
QY	337	CTGCTGGGAGCAACCGAAGAAAGCCCTTCCCTGGTGGCTGCTGATGCTGGATGA	396
DB	1407	CTGCTGGGAGCAACCGAAGAAAGCCCTTCCCTGGTGGCTGCTGATGCTGGATGA	1466
QY	397	CCGAGTTAACAGGCGCGTGTGGCTGTCTGTAAGCCAAAGTGGGCGAGCCCTGGCAG	456
DB	1467	CCGAGTTAACAGGCGCGTGTGGCTGTCTGTAAGCCAAAGTGGGCGAGCCCTGGCAG	1526
QY	457	ATGACCTGCGAAGGGGCCCTGTCTTCCAGGCCCCCAACCACTAGAGCTTGAGGCTCT	516
DB	1527	ATGACCTGCGAAGGGGCCCTGTCTTCCAGGCCCCCAACCACTAGAGCTTGAGGCTCT	1586
QY	517	TTTCGGGCGCAAGTTCCTCTAGTGGCCCTCCACAGCCGACCTTCCCTCTACCTCGAGGCC	576
DB	1587	TTTCGGGCGCAAGTTCCTCTAGTGGCCCTCCACAGCCGACCTTCCCTCTACCTCGAGGCC	1646
QY	577	AAGAGAGAGAGCGAGAGTGGGAAAGCTCTGCTGCCATGATGCTGCTCTCGAAG	636
DB	1647	AAGAGAGAGAGCGAGAGTGGGAAAGCTCTGCTGCCATGATGCTGCTCTCGAAG	1706
QY	637	GCTGGCTGGGATGAGAGCTTCCGGGGCATGCTGGGCGAAGTCCCTGACTCTGTGACCTG	696
DB	1707	GCTGGCTGGGATGAGAGCTTCCGGGGCATGCTGGGCGAAGTCCCTGACTCTGTGACCTG	1766
QY	697	CCCGGCGCAGCTGACACCTGAGCTGTCTGAGAGCCCTTGGGTTTGTGTTGTTG	756
DB	1767	CCCGGCGCAGCTGACACCTGAGCTGTCTGAGAGCCCTTGGGTTTGTGTTGTTG	1826
QY	757	TTTGTGTTGTTGTTGTTTCTCCCTGGGCTCTGCCAGCTCTGAGCTTCCAGAAACCC	816
DB	1827	TTTGTGTTGTTGTTGTTTCTCCCTGGGCTCTGCCAGCTCTGAGCTTCCAGAAACCC	1886

QY	817	CAGATCTCTTCTGAGAGAGGAGCTTCTGAGAGAGGAGATGCTGAGTCAACCAT	876
DB	1887	CAGATCTCTTCTGAGAGAGGAGCTTCTGAGAGAGGAGATGCTGAGTCAACCAT	1946
QY	877	GAAGACAGGACAGCTGCTTCCAGCTGAGAGCTGCGGAGATGCTTGGGCTCTGTG	936
DB	1947	GAAGACAGGACAGCTGCTTCCAGCTGAGAGCTGCGGAGATGCTTGGGCTCTGTG	2006
QY	937	TAGGAGAGAGTGGGAGCCCTGAGGAAACGGGCTCTCAAGTTAGCTCAGAGAGCTTG	996
DB	2007	TAGGAGAGAGTGGGAGCCCTGAGGAAACGGGCTCTCAAGTTAGCTCAGAGAGCTTG	2066
QY	997	GAAAGCATCACTCAGGCGCAGGTGAGTGGCTCAGCCCTATGATCCACACTTTGGGAG	1056
DB	2067	GAAAGCATCACTCAGGCGCAGGTGAGTGGCTCAGCCCTATGATCCACACTTTGGGAG	2126
QY	1057	GCTGAGGCGGGTGGATCACCCTGAGGTTAGAGCTTGAGACAGACCTTGCCCAATGTAA	1116
DB	2127	GCTGAGGCGGGTGGATCACCCTGAGGTTAGAGCTTGAGACAGACCTTGCCCAATGTAA	2186
QY	1117	AACCCATCTCTTAATAATACAGAAATTAGCCGGGCTGGTGGCGGACACTATAGTC	1176
DB	2187	AACCCATCTCTTAATAATACAGAAATTAGCCGGGCTGGTGGCGGACACTATAGTC	2246
QY	1177	CCAGCTACTCAGAGGCTGAGGCTGGAAATGTTTGAACCCGGGAGCGGAGTTGCGAG	1236
DB	2247	CCAGCTACTCAGAGGCTGAGGCTGGAAATGTTTGAACCCGGGAGCGGAGTTGCGAG	2306
QY	1237	GGAGCGGATACAGGCGCATGTCACATCCCTGGGCGACAGAGAGTCTGTCAAA	1296
DB	2307	GGAGCGGATACAGGCGCATGTCACATCCCTGGGCGACAGAGAGTCTGTCAAA	2366
QY	1297	AGAAAAAAGAACACACCGCTCCAAATGCTAACCTTGTCTTTGTACATGCTGTAA	1356
DB	2367	AGAAAAAAGAACACACCGCTCCAAATGCTAACCTTGTCTTTGTACATGCTGTAA	2426
QY	1357	AGTCAGATCCCGAGAGGCGCCAGGCGACAGGCGACATATTGAGTGTGGCTGGCAAGA	1416
DB	2427	AGTCAGATCCCGAGAGGCGCCAGGCGACAGGCGACATATTGAGTGTGGCTGGCAAGA	2486
QY	1417	TACGCACTTCTAATAGAAATCTGCCAATTTTAAAAAGTAGTACCACTAGGCCA	1476
DB	2487	TACGCACTTCTAATAGAAATCTGCCAATTTTAAAAAGTAGTACCACTAGGCCA	2546
QY	1477	ACAAGCGAAGCAAAAGCCAACTCTGCCAGCAGACATCAACCCCGACCTGCCATTGGC	1536
DB	2547	ACAAGCGAAGCAAAAGCCAACTCTGCCAGCAGACATCAACCCCGACCTGCCATTGGC	2606
QY	1537	ACCCTCGGCTTCACTCCGGTGTGCTGCTGAGCCCGGCTCTCTTCTGCTGTCTAGG	1596
DB	2607	ACCCTCGGCTTCACTCCGGTGTGCTGCTGAGCCCGGCTCTCTTCTGCTGTCTAGG	2666
QY	1597	CCACACATCTCTCTTTCAGGAAATTTAGAACTAGAGATGAGTGCCTGTAAGCAT	1656
DB	2667	CCACACATCTCTCTTTCAGGAAATTTAGAACTAGAGATGAGTGCCTGTAAGCAT	2726
QY	1657	CTCTTACTTCTACTCTAGCTTACACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTTC	1716
DB	2727	CTCTTACTTCTACTCTAGCTTACACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTTC	2786
QY	1717	CCCACTCCCACTTCAATTCCTGGGCGCCAAAGGGGTGGCCCTGCCACTTGTATATG	1776
DB	2787	CCCACTCCCACTTCAATTCCTGGGCGCCAAAGGGGTGGCCCTGCCACTTGTATATG	2846
QY	1777	GCCAGTGTGATCCCAAGTGCAGTCTGTGCTGCTGCTGTGCTGTGCTGTGCTGTG	1836
DB	2847	GCCAGTGTGATCCCAAGTGCAGTCTGTGCTGCTGCTGTGCTGTGCTGTGCTGTG	2906
QY	1837	TGTAGCCAAAGTGGTAAAGTTGGAATGGCTGTGCTTGAAGCCACTGAAGCTGGATTCTTC	1896
DB	2907	TGTAGCCAAAGTGGTAAAGTTGGAATGGCTGTGCTTGAAGCCACTGAAGCTGGATTCTTC	2966
QY	1897	CCCATTAGAGTCAAGCTTCCCTCCAGGCGCAGGCGCTCGCAGAGAGGGAACCACTGT	1956

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Db 2967 CCCATTAGAGTACAGCTTCCCTCCAGAGGCCAGGCGCTCCAGAGGGGAAACAGTGT 3026
Oy 1957 AGCCCTTGGCCGGATTTCTGGAGAGAGCGTTGAGGGCTCTCGAAAGGCTCACTCTCA 2016
Db 3027 AGCCTTGGCCGGATTTCTGGAGAGAGCGTTGAGGGCTCTCGAAAGGCTCACTCTCA 3086
Oy 2017 GGAGCATGGGATTAAGAGAGAGCATGAATGTCTAGACAGAGGAGGCGAGGTGATA 2076
Db 3087 GGAGCATGGGATTAAGAGAGAGCATGAATGTCTAGACAGAGGAGGCGAGGTGATA 3146
Oy 2077 AATTGTGATTAATTCACACTGACCTTGACCTTGACCTGAACTATTGAGAGGGTGAGGA 2136
Db 3147 AATTGTGATTAATTCACACTGACCTTGAGCTTGAGCTGAACTATTGAGAGGGTGAGGA 3206
Oy 2137 GCCCAGCCATTACATGAGACAGAGAGGTTTCCACCTGGGAATCAAGATGTCAGACT 2196
Db 3207 GCCCAGCCATTACATGAGACAGAGAGGTTTCCACCTGGGAATCAAGATGTCAGACT 3266
Oy 2197 GCGTGGCTGCACTGACGTCGACCTTACTCAGAGAGGCTGAGGGAGATCACTGAGGCC 2256
Db 3267 GCGTGGCTGCACTGACGTCGACCTTACTCAGAGAGGCTGAGGGAGATCACTGAGGCC 3326
Oy 2257 AGGAGTTGAGGCTGACGAGGACTGATGTCGCGCCACTACACTCAGCTGAGCAACAGA 2316
Db 3327 AGGAGTTGAGGCTGACGAGGACTGATGTCGCGCCACTACACTCAGCTGAGCAACAGA 3386
Oy 2317 GTGAGACCCCTGTCTCTTAAGAAAAAAGTCAAGACTGTGGGAGCTGGCAGGTTTCTG 2376
Db 3387 GTGAGACCCCTGTCTCTTAAGAAAAAAGTCAAGACTGTGGGAGCTGGCAGGTTTCTG 3446
Oy 2377 CCCAATTGGAGCCCATGAGAGACATGATGAGAGCGCACCTGCCCCCTGGTGAGACATCTT 2436
Db 3447 CCCAATTGGAGCCCATGAGAGACATGATGAGAGCGCACCTGCCCCCTGGTGAGACATCTT 3506
Oy 2437 GGGAGAACCTGAGGCTTCTGGCATCACAGGAGAGCGGAGAGGAGATGATTTGGAG 2496
Db 3507 GGGAGAACCTGAGGCTTCTGGCATCACAGGAGAGCGGAGAGGAGATGATTTGGAG 3566
Oy 2497 ACTCTGTGGGGCTTGGTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2556
Db 3567 ACTCTGTGGGGCTTGGTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3626
Oy 2557 CACTGTATGCTGAGAGGATTCCTGCTTATCAATAAACCTGTTTGTAAAAAAA 2613
Db 3627 CACTGTATGCTGAGAGGATTCCTGCTTATCAATAAACCTGTTTGTAAAAAAA 3683

RESULT 6
ABK33467
ID ABK33467 standard; DNA: 3683 BP.
XX
AC ABK33467;
Df 23-APR-2002 (first entry)
XX
Df Human TNF receptor II gene with SNP in exon 6.
XX
Km Human: anti-tumour necrosis factor receptor II; TNF receptor II; SNP.
Km Chromosome 1p36; Influximab therapy; Crohn's disease; malignant disorder;
Km Inflammatory disorder; chronic disease; receptor; gene;
XX Single nucleotide polymorphism; ds.
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OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT mat_peptide 156..1472
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PN EPI172444-A1.
PD 16-JAN-2002.
PE 10-JUL-2000; 2000EP-0114786.
PR 10-JUL-2000; 2000EP-0114786.
PA (CONA-) CONARIS RES INST GMBH.
PI Schreiber S, Hampe J, Mascheretti S;
DR WPI: 2002-156651/21.
DX P-PSDB; AA075174.
XX
PT Detecting non-responders to anti-human necrosis factor therapy,
PT compares testing an individual for homozygosity for a single
PT nucleotide polymorphism in the gene coding for the tumour necrosis
PT factor receptor II -
XX
PS Claim 16; Page 35-39; 45pp; English.
XX
CC The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC Met16Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC Influximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC represents the human TNF receptor II gene containing the SNP in exon 6.
XX
SQ Sequence 3683 BP; 780 A; 1098 C; 1088 G; 717 T; 0 other;

Query Match 95.4%; Score 2493; DB 24; Length 3683;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 97 GACCCCCACCCCATCTTGTGCTTAGCAGATCTTCCCTCGTGGCCATGAGGCCACAGTTC 156
Db 1167 GAGGCCCGGGCCAGACCCGGAGACTAGATTTCTTCCCTGTGGCCATGAGGCCACAGTTC 1226
Oy 157 AATGTACCTGATCGTGAAGCTGTGTAGACAGCTGTGACACAGCTCAAGTGTCTCTCC 216
Db 1227 AATGTACCTGATCGTGAAGCTGTGTAGACAGCTGTGACACAGCTCAAGTGTCTCTCC 1286
Oy 217 CAAGCAGCTCCACAAATGGAGACACAGATTCCAGCCCTCGGAGTCCCGAAGAGCAG 276
Db 1287 CAAGCAGCTCCACAAATGGAGACACAGATTCCAGCCCTCGGAGTCCCGAAGAGCAG 1346
Oy 277 CAGGTCCCTTCCCAAGAGAGATGTGCTTGGGTACACAGCTGAGAGAGCGAGAGACC 336
Db 1347 CAGGTCCCTTCCCAAGAGAGATGTGCTTGGGTACACAGCTGAGAGAGCGAGAGACC 1406
Oy 337 CTGCTGGGAGACCGAAGAGAGCCCTGCCCCCTGTGAGTGCCTGATCTGGATGAG 396
Db 1407 CTGCTGGGAGACCGAAGAGAGCCCTGCCCCCTGTGAGTGCCTGATCTGGATGAG 1466
Oy 397 CCCAGTTAACGAGCGCGGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 456
Db 1467 CCCAGTTAACGAGCGCGGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1526
Oy 457 ATGACCTTGCAGAGGGGCTTGTCTTCCAGAGGCCCCACACACTAGAGACTGTGAGGCTCT 516
Db 1527 ATGACCTTGCAGAGGGGCTTGTCTTCCAGAGGCCCCACACACTAGAGACTGTGAGGCTCT 1586
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Oy	517	TTCTGGGGCCAAAGTTTCCCTTCAAGTGGCCCTCCACAGCCGCAAGCCTCCCTCTGACCTGCAGGCC	576
Db	1587	TTCTGGGCCAAAGTTTCTCTTAAGTGGCCCTCCACAGCCGCAAGCCTCCCTCTGACCTGCAGGCC	1644
Oy	577	AAGAGCAGAGAGCCAGCCAGTGTGGGAAACCTCTGTCGCAATGGGTGTCCCTCTGGGAG	636
Db	1647	AAGAGCAGAGAGCCAGCGAGTGTGGGAAACCTCTGTCGCAATGGGTGTCCCTCTGGGAG	1706
Oy	637	GCTGGCTGGGCATGGACGTTCCGGGCATGCTGGGGCAAGTCCCTGACCTCTGTGACCTG	696
Db	1707	GCTGGCTGGGCATGGACGTTCCGGGGCAAGTCCCTGACCTCTGTGACCTG	1766
Oy	697	CCCCGCCACAGCTGCACCTGCCAGCCTGGCCTTCTGAGACCCCTTGGGATTTTGTGTGTTG	756
Db	1767	CCCCGCCACAGCTGCACCTGCCAGCCTGGCCTTCTGAGACCCCTTGGGATTTTGTGTGTTG	1826
Oy	757	TTTTGTTTGTTTGTTTGTTTCTTCCCTCGGCTGTGCCACCTGTGCCTTCAGAAAAACC	816
Db	1827	TTTTGTTTGTTTGTTTGTTTCTTCCCTCGGCTGTGCCACCTGTGCCTTCAGAAAAACC	1886
Oy	817	CAGCATCTCTTTCTGCAGAGGGGCTTCTGGAGAGGGAGATGCTGCTGATCACCAT	876
Db	1887	CAGCATCTCTTTCTGCAGAGGGGCTTCTGGAGAGGGAGATGCTGCTGATCACCAT	1946
Oy	877	GAAGACAGACAGTCTCTTACCTTCAGCCTGAGACCTGCGAGATGCTCGGCGCTGTG	936
Db	1947	GAAGACAGACAGTCTCTTACCTTCAGCCTGAGACCTGCGAGATGCTCGGCGCTGTG	2006
Oy	937	TAGGGAGAGGAGTGGAGCCCTGTAGGAGAAAGGGGTCTTCAAGTTAGCTCAGAGGCTTG	996
Db	2007	TAGGGAGAGGAGTGGAGCCCTGTAGGAGAAAGGGGTCTTCAAGTTAGCTCAGAGGCTTG	2066
Oy	997	GAAGACATACCTCAGGCCAGGTGCAGTGGCTACGCCCTATGATCCAGACATTTGGAG	1056
Db	2067	GAAGACATACCTCAGGCCAGGTGCAGTGGCTACGCCCTATGATCCAGACATTTGGAG	2126
Oy	1057	GCTGAGGGGGGTGGATCACCCTGAGAGTTAGAGTTTCAAGACACAGCTGGCCAACTGGTAA	1116
Db	2127	GCTGAGGGGGGTGGATCACCCTGAGAGTTAGAGTTTCAAGACACAGCTGGCCAACTGGTAA	2186
Oy	1117	AAACCCATCTCTACTAAATAATACGAATAATAGCCGGGCTGGTGGCGGACATATAGTC	1176
Db	2187	AAACCCATCTCTACTAAATAATACGAATAATAGCCGGGCTGGTGGCGGACATATAGTC	2246
Oy	1177	CCAGCTACTCAGAAAGCCTGAGGCTGGGAAATGCTTTGAACCCGGGAGCGGAGGTTGCAG	1236
Db	2247	CCAGCTACTCAGAAAGCCTGAGGCTGGGAAATGCTTTGAACCCGGGAGCGGAGGTTGCAG	2306
Oy	1237	GGAGCCGAGATCAGGCGCAGTGCACCTCAGCCTGAGGCGAGAGGCGAGAGTGTCTCAA	1296
Db	2307	GGAGCCGAGATCAGGCGCAGTGCACCTCAGCCTGAGGCGAGAGGCGAGAGTGTCTCAA	2366
Oy	1297	AGAAAAAAGAAAAAGCAGCGGCTCCAAATGCTAACTGTGCTTTTGTACATGGTGTGAA	1356
Db	2367	AGAAAAAAGAAAAAGCAGCGGCTCCAAATGCTAACTGTGCTTTTGTACATGGTGTGAA	2426
Oy	1357	AGTCAGATGGCCAGAGAGGCCAGGCGGCGACCATATTCAGTGTGTGGCTGGGCAAGA	1416
Db	2427	AGTCAGATGGCCAGAGAGGCCAGGCGGCGACCATATTCAGTGTGTGGCTGGGCAAGA	2486
Oy	1417	TACGCACTTCTAAGTAATCTGGCAATTTTAAAAAAGTAAGTAAACACTCAGGCC	1476
Db	2487	TACGCACTTCTAAGTAATCTGGCAATTTTAAAAAAGTAAGTAAACACTCAGGCC	2546
Oy	1477	ACAAGCCAGACAAAAAGCCAAACTGTCCAGGCAATCACAACCCGCCACCTGCCATTGCG	1536
Db	2547	ACAAGCCAGACAAAAAGCCAAACTGTCCAGGCAATCACAACCCGCCACCTGCCATTGCG	2606
Oy	1537	ACGCTCGGCTTCACTCGGCTGTGCTGCAGAGCCCGCGCTCTCTTCTGTCTGTCTAGG	1596
Db	2607	ACGCTCGGCTTCACTCGGCTGTGCTGCAGAGCCCGCGCTCTCTTCTGTCTGTCTAGG	2666
Oy	1597	CCACACATCTCTTTCAGGGAATTTCAAGAACTAGAGATGACTGAGTCTCTGTAGCCAT	1656

Db	2667	CCACACCATCTCCTTTCCAGGAAATTTCAAGAACTAGAGAAAGTACGATGCTCTGTAGCCAT	1718
Qy	1657	CTCTCTACTCTTACCTCAACCTTAGACCTCTCTCTCCCCAGAGGGGTGGTTCTCTTC	1718
Db	2727	CTCTCTACTCTCTACCTCAACCTTAGACCTCTCTCTCTCTCCCCAGAGGGGTGGTTCTCTTC	2786
Qy	1717	CCCACTCCCACTTCAAATTCCTGGGGCCCCAAACGGCTCTCCTGCCACTTTGGTATAG	1717
Db	2787	CCCACTCCCACTTCAAATTCCTGGGGCCCCAAACGGCTCTCCTGCCACTTTGGTATAG	2846
Qy	1777	GCCAGTGTGATCCCAAGTCCAGTCTTGTCGTCTGCTCTGTGTGGCTGTGGGTG	1836
Db	2847	GCCAGTGTGATCCCAAGTCCAGTCTTGTCGTCTGCTCTGTGTGGCTGTGGGTG	2906
Qy	1837	TGTAGCCAAAGTCCGCTTAAGTTGATGGCTGTGCTTGAAGCACTGAAGCTGGATTCTTC	1896
Db	2907	TGTAGCCAAAGTCCGCTTAAGTTGATGGCTGTGCTTGAAGCACTGAAGCTGGATTCTTC	2966
Qy	1897	CCCATTTAGAGTAGAGCTTTCCTCCCTCCAGGGCCAGGGCCCTGTGAGGGGAAACAGTGT	1956
Db	2967	CCCATTTAGAGTAGAGCTTTCCTCCCTCCAGGGCCAGGGCCCTGTGAGGGGAAACAGTGT	3026
Qy	1957	AGCTTTGCCCGGATTTCTGGAGGAAGAGGTTGAGGGGCTCTCTGAAAGGCTCAAGTCA	2016
Db	3027	AGCTTTGCCCGGATTTCTGGAGGAAGAGGTTGAGGGGCTCTCTGAAAGGCTCAAGTCA	3086
Qy	2017	GGAGCATGGGGATTAAGGAGAAGGCATGAATTTGTACACAGCAGGGCCAGGGTGATA	2076
Db	3087	GGAGCATGGGGATTAAGGAGAAGGCATGAATTTGTACACAGCAGGGCCAGGGTGATA	3146
Qy	2077	AATTTGTGATAAATTTCCACTGTGAGTTGAGCTTGGAGCTTGTGAGAGGGGGAGA	2136
Db	3147	AATTTGTGATAAATTTCCACTGTGAGTTGAGCTTGGAGCTTGTGAGAGGGGGAGA	3206
Qy	2137	GGCCAGCCATTTCATGATGAGACAAAGAAGGTTTTTCACCCCTGGAATCAAGATGTTCAGACT	2196
Db	3207	GGCCAGCCATTTCATGATGAGACAAAGAAGGTTTTTCACCCCTGGAATCAAGATGTTCAGACT	3266
Qy	2197	GGCTGGCTGCAGTACAGTGCACCTGTACTAGAGGCTGAGGGAGATTCACGTGAGCC	2256
Db	3267	GGCTGGCTGCAGTACAGTGCACCTGTACTAGAGGCTGAGGGAGATTCACGTGAGCC	3326
Qy	2257	AGGAGTTTGAAGCTGCAGCGAGCTATGATCGGCCACTAACATCCAGCCTGAGCAACAGA	2316
Db	3327	AGGAGTTTGAAGCTGCAGCGAGCTATGATCGGCCACTAACATCCAGCCTGAGCAACAGA	3386
Qy	2317	GGGAGACCCCTCTCTTAAAGAAAAAAAGTCACTGTGGGACTGTGGCAGGTTTTCTG	2376
Db	3387	GGGAGACCCCTCTCTTAAAGAAAAAAAGTCACTGTGGGACTGTGGCAGGTTTTCTG	3446
Qy	2377	CCCACTTGGACCCACATGTAGACATGATGAGAGGCACTGCCCCCTGTGTGACAGTCTCT	2436
Db	3447	CCCACTTGGACCCACATGTAGACATGATGAGAGGCACTGCCCCCTGTGTGACAGTCTCT	3506
Qy	2437	GGGAGAACCTTAGGCTTCTTGGCATCACAGGGCAGAGCCGGGAAGGATGAATTTGGAG	2496
Db	3507	GGGAGAACCTTAGGCTTCTTGGCATCACAGGGCAGAGCCGGGAAGGATGAATTTGGAG	3566
Qy	2497	ACTGTGTGGGGCTTGGTTCCCTGTGTGTGTGTGTATATCCCAAGCAATGAAGTTTG	2556
Db	3567	ACTGTGTGGGGCTTGGTTCCCTGTGTGTGTGTGTATATCCCAAGCAATGAAGTTTG	3626
Qy	2557	CACGTATGCTGGAGCGCATCTCTGCTATCAATTAACCTTTGTTTAAAAAAA	2613
Db	3627	CACGTATGCTGGAGCGCATCTCTGCTATCAATTAACCTTTGTTTAAAAAAA	3683
RESULT 7			
AAQ10956			
TX ---AAQ10956 standard; DNA: 2339 BP.			
AAQ10956:			

```
XX 24-MAY-1991 (first entry)
DT Encodes human 75kd TNF-binding protein.
XX
DE Tumour Necrosis Factor: binding proteins; septic shock;
XX autoimmune glomerulonephritis; lymphokine; cytokine.
XX
FH Key Location/Qualifiers
FT CDS 1..1179
FT /tag= a
FT /product= 75kd TNF-BP
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XX EPA17563-A.
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XX 12-SEP-1989: 89CH-0003319.
XX 08-MAR-1990: 90CH-0000746.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Brockhaus M, Demble Z, Gentz R, Lesslauer W, Lotscher H;
XX Schlieger EJ;
XX
XX WPI: 1991-081851/12.
XX P-PSDU: AAR11605.
XX
XX Insoluble tumour necrosis factor binding proteins - and DNA
XX encoding them, useful in pharmaceutical prods. and for antibody
XX prodn.
XX
XX Claim 4: Fig 1: 26pp; German.
XX
XX Partial amino acid sequences were determined for the 55 and 75KD
XX TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
XX synthesised based on these partial sequences. The primers were
XX used to produce a cDNA fragment for use as a probe to screen a human
XX placental cDNA bank constructed in lambda g11. Positive clones were
XX identified and sequenced. Repeated sequencing showed a discrepancy
XX at position 7 such that the third codon encodes either Thr or Ser.
XX cDNA constructs comprising the TNF-BP coding sequence may also
XX contain a fragment encoding a human Ig domain. Recombinant
XX constructs are used to transform cells to confer improved TNF-
XX binding properties.
XX See also AAQ10955.
XX
XX
XX Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other:
XX
XX Query Match 54.5%; Score 1423; DB 12; Length 2339;
XX Best Local Similarity 98.5%; Pred. No. 0;
XX Matches 1457; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
XX
XX
XX 89 CCGGAGTGAAGCCCAACCCATCTGTGCTAGACAGATTCTCCCTGTGGCCATGGGA 148
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 863 CCGGGAGGCGCCGGGCGAGACCGGAGCTCAGCAGATTCTTCCCTGTGGCCATGGGA 922
XX
XX 149 CCAGAGTCAATGTACCTGCATCGATGTAACGCTGTAGACAGCTGTACCAAGCTTACAGT 208
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 923 CCAGAGTCAATGTACCTGCATCGTGAAGCTGTAGACAGCTGTACCAAGCTTACAGT 982
XX
XX 209 GCTCTCTCCCAAGCCAGCTGCACATGAGGAGACAGATTCCAGCCCTCGGAGTCCCGGA 268
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 983 GCTCTCTCCCAAGCCAGCTGCACATGAGGAGACAGATTCCAGCCCTCGGAGTCCCGGA 1042
XX
XX 269 AGAGCAGCAGAGTCCCTTCTCCAAAGAGAAATGTCCCTTTCGGTCAACAGCTGGAGAGC 328
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1043 AGAGCAGCAGAGTCCCTTCTCCAAAGAGAAATGTCCCTTTCGGTCAACAGCTGGAGAGC 1102
XX
XX 329 CAGAGACCTGCTGGGAGACACCGAAGAGAGCCCTCTGCCCCCTTGAGAGTGCCTGATGCTG 388
XX
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Db 1103 CAGAGACCTGCTGGGAGACACCGAAGAGCCCTTGCCCTTGAGAGTGCCTGATGCTG 1162
XX || || || || || || || || || || || || || || || || || || || ||
XX
XX 389 GGATGAAGCCAGTTAAACACGCGGCTGTGGCTGTCTGTAGCAAGTGGGCTAGCC 448
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XX Db 1163 GGATGAAGCCAGTTAAACACGCGGCTGTGGCTGTCTGTAGCAAGT-6GCTAGGCC 1221
XX
XX 449 CTGGCAGATGATACCTTGGGAAGGGGCCCTGGTCTTCCAGAGCCCAACCACTAGAGACTCT 508
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1222 CTGGCAGATGATACCTTGGGAAGGGGCCCTGGTCTTCCAGAGCCCAACCACTAGAGACTCT 1281
XX
XX 509 GAGGCTCTTTTGGGCCCAAGTTCTCTAGTCCCTCCACAGCCGACAGCCCTCCCTGAGC 568
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1282 GAGGCTCTTTTGGGCCCAAGTTCTCTAGTCCCTCCACAGCCGACAGCCCTCCCTGAGC 1341
XX
XX 569 TGCAGGCCAAGAGCAGAGCCAGGAGTTGGGAAAGCTCTGCTGCCATGTGTGCTCCT 628
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1342 TGCAGGCCAAGAGCAGAGCCAGGAGTTGGGAAAGCTCTGCTGCCATGTGTGCTCCT 1401
XX
XX 629 CTGGGAAGGCTGGCTGGGCAATGACGTTTCGGGCAATGCTGGGCAAGTCCCTGACTCTCT 688
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1402 CTGGGAAGGCTGGCTGGGCAATGACGTTTCGGGCAATGCTGGGCAAGTCCCTGACTCTCT 1461
XX
XX 689 GTGACCTGGCCCCGCGCAGCTGCACTGCGACCTGGCTTCTGGAGCCCTTGGGCTTTTGG 748
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1462 GTGACCTGGCCCCGCGCAGCTGCACTGCGACCTGGCTTCTGGAGCCCTTGGGCTTTTGG 1521
XX
XX 749 TTTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 808
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1522 TTTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1581
XX
XX 809 GAAACCCCAAGCATCTTTCTGCAAGAGGCGCTTTTGGAGAGAGAGATGCTGCTGATG 868
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1582 GAAACCCCAAGCATCTTTCTGCAAGAGGCGCTTTTGGAGAGAGAGATGCTGCTGATG 1641
XX
XX 869 TCACCATGAAGACAGACAGTCTCAGCGTTAGAGCTGAGACTGGGGATGATGCTCTGG 928
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XX
XX 929 GCTGTGTGAGGAGAGAGTGGGAGCCCTGTAGAGAACGGGCTCTTCAAGTTTACCTAG 988
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XX 989 GAGGCTTGAAGACATACCTCAGCGCAGGTGAGGGCTCAGGCTTATGATCCAGAC 1048
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XX
XX 1049 TTTGGAGGCTGAGCGGGGTGATCAGTGAAGTTAGAGTTCAGAGACCACTGGCCAA 1108
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1822 TTTGGAGGCTGAGCGGGGTGATCAGTGAAGTTAGAGTTCAGAGACCACTGGCCAA 1881
XX
XX 1109 CATGGTAAAAACCCATCTCTACTATAAAATACGAATTAAGCCGGGCTGTGGCGGCAC 1168
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1882 CATGGTAAAAACCCATCTCTACTATAAAATACGAATTAAGCCGGGCTGTGGCGGCAC 1941
XX
XX 1169 CTATTAGTCCAGTACTCAGAAAGCTGAGGCTGGGAAATCGTTTGAACCCGGGAAGGGA 1228
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 1942 CTATTAGTCCAGTACTCAGAAAGCTGAGGCTGGGAAATCGTTTGAACCCGGGAAGGGA 2001
XX
XX 1229 GGTTCAGGAGACCGAGATCAGACGCACTGCACTCCAGCTTGGGCGACAGAGCGAGAGTCT 1288
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 2002 GGTTCAGGAGACCGAGATCAGACGCACTGCACTCCAGCTTGGGCGACAGAGCGAGAGTCT 2061
XX
XX 1289 GTCTCAAAAGAAAAAAGCACCCTCTCAAAATGCTTAATCTGTGTCCTTTTGTACCAT 1348
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 2062 GTCTCAAAAG-AAAAAAGAAAAAGCACCCTCTCAAAATGCTTAATCTGTGTCCTTTTGTACCAT 2120
XX
XX 1349 GGTGTGAAGTACATGCCCAGAGAGGCGCCAGGAGCCACCATTTTCAAGTGTGTGGCT 1408
XX || || || || || || || || || || || || || || || || || || || ||
XX Db 2121 GGTGTGAAGTACATGATGCCAGAGGCGCCAGGAGCCACCATATTTCAAGTGTGTGGCT 2180
XX
XX 1409 GGGCAAGATACGCACTTCTAAGTAAGATGCAATTTTTTAAAAAGTAAGTACAC 1468
XX || || || || || || || || || || || || || || || || || || || ||
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Query Match	54.5%;	Score 1423;	DB 20;	Length 2339
Best Local Similarity	98.5%;	Pred. NO. 0;		

[illegible]

1002 CAGGACCCATCTTAAATAACAGAATTAGCCGGCGGTGGTGCGGCAC 1941

Query Match	Best Local Similarity	54.5% Matches 1457; Conservative	Score 1423; 0; Mismatches	DB 22; 20; Indels	Length 2339; 2; Gaps
PS	Claim 4a: Fig 4; 26pp: German.				
PT	(TNF), useful for treating TNF-mediated disorders, e.g. inflammation				
XX					
XX	This invention describes novel insoluble proteins (I), also their				
CC	(in)soluble fragments and pharmaceutically acceptable salts, able to bind				
CC	tumor necrosis factor (TNF) and in homogeneous form. The products of the				
CC	invention have antiinflammatory, immunosuppressive, antibacterial,				
CC	antiparasitic activity (I), and related recombinant proteins, are used				
CC	to treat diseases mediated by TNF, e.g. shock in cases of meningococcal				
CC	sepsis; development of autoimmune glomerulonephritis and cerebral				
CC	malacia. Also (I), or antibodies specific for them, are used for				
CC	diagnostic determination of TNF in body fluids, for affinity purification				
CC	of TNF and for identifying (antagonists of TNF. This sequence encodes a				
CC	human TNF binding protein described in the method of the invention.				
XX					
XX					
SQ	Sequence 2339 BP: 494 A; 720 C; 685 G; 440 T; 0 other:				
Query Match	54.5% Best Local Similarity	Score 1423; Matches 1457; Conservative	DB 22; 0; Mismatches	Length 2339; 20; Indels	2; Gaps
QY	89	CCCGCAGTACGCCCCACCCCACTCTTGTGCTTACACATTTCTTCCCTGTGGCCATGGGA	148		
Db	863	CCGGGAGAGCCCGGGGACACGACGGGAGCTACACAAATTTCTTCCCTGTGGCCATGGGA	922		
QY	149	CCGAGTCAATGTCACTGCATGCTGAACCTCTGTAGCAGCTGTGACACAGCTCACAGT	208		
Db	923	CCGAGTCAATGTCACTGCATGCTGAACCTCTGTAGCAGCTGTGACACAGCTCACAGT	982		
QY	209	GCTCTCCCAAGCCAGCTCCACCAATGGGAGACACAGATCCAGCCCTCGGAGTCCCGGA	268		
Db	983	GCTCTCCCAAGCCAGCTCCACCAATGGGAGACACAGATCCAGCCCTCGGAGTCCCGGA	1042		
QY	269	AGACGACAGAGTCCCTTCTCCAAAGAGAAATGTGCTTTCGTGTCACAGTGGAGACGC	328		
Db	1043	AGACGACAGAGTCCCTTCTCCAAAGAGAAATGTGCTTTCGTGTCACAGTGGAGACGC	1102		
QY	329	CAGAGACCCCTCTGGGGAGACGACCAAGACAAACCCCTGCGCTTGTGAGTGCCTGATCTG	388		
Db	1103	CAGAGACCCCTCTGGGGAGACGACCAAGACAAACCCCTGCGCTTGTGAGTGCCTGATCTG	1162		
QY	389	GGATGAAACCCAGTTAAACAGGCGGTGTGGGCTGTGTCAGTACGCAAGTGGGCTGAGCC	448		
Db	1163	GGATGAAACCCAGTTAAACAGGCGGTGTGGGCTGTGTCAGTACGCAAGTGGGCTGAGCC	1221		
QY	449	CTGGAGAGATGACCCCTCGGAGGAGGCGCTGTGCTTCCAGGCCCCCAACACTAGACTCT	508		
Db	1222	CTGGAGAGATGACCCCTCGGAGGAGGCGCTGTGCTTCCAGGCCCCCAACACTAGACTCT	1281		
QY	509	GAGGCTCTTCTGTGGGCAAGTTCTCTATGTGCCCTCCACAGCCCGCAGCTCTGTGACC	568		
Db	1282	GAGGCTCTTCTGTGGGCAAGTTCTCTATGTGCCCTCCACAGCCCGCAGCTCTGTGACC	1341		
QY	569	TGCAGGCGCAAGACACAGGACAGAGTGTGGGAAAGCCTCTGCTGCCATGTTGTCCCT	628		
Db	1342	TGCAGGCGCAAGACACAGGACAGAGTGTGGGAAAGCCTCTGCTGCCATGTTGTCCCT	1401		
QY	629	CTGCGAAGCTGTGCTGGGATGAGACTTCGCGGAGCATGCTGGGAGCAATCCCTACACTCT	688		
Db	1402	CTGCGAAGCTGTGCTGGGATGAGACTTCGCGGAGCATGCTGGGAGCAATCCCTACACTCT	1461		
QY	689	GTCGACCTGCCCCCGCCAGCTGACCTGGCAGCCTTGCTTGTGAGGCCCTTGGGTTTTTGG	748		
Db	1462	GTCGACCTGCCCCCGCCAGCTGACCTGGCAGCCTTGCTTGTGAGGCCCTTGGGTTTTTGG	1521		
QY	749	TTTGTGTTGTTGTTGTTGTTGTTGTTTCTCCCTCGGGCTCTGCCAGCTGTGGCTTCCA	808		
Db	1522	TTTGTGTTGTTGTTGTTGTTGTTGTTTCTCCCTCGGGCTCTGCCAGCTGTGGCTTCCA	1581		
QY	809	GAAGAACCCAGCATCTTCTTCGACAGAGGGCTTTCGAGACGAGGATGCTGCTTGAG	868		
Db	1582	GAAGAACCCAGCATCTTCTTCGACAGAGGGCTTTCGAGACGAGGATGCTGCTTGAG			

PR	18-JUL-1989;	8905-0381080.
PR	11-DEC-1989;	8905-0450329.
PR	07-FEB-1990;	9005-0479661.
PA	(AMGE-) AMGEN INC.	
XX		
PI	Squires C, King MW, Hale KK, Brewer MT, Thompson RC;	
PI	Vanderstille RW, Vannice J, Kohno T;	
DR	MDI; 2001-006443/01.	
DR	P-PSDB; AAB37686.	
XX		
PT	Novel 30 kDa tumor necrosis factor inhibitor analog comprising a	
PT	non-native cysteine residue cross-linked with polyethylene glycol,	
PT	useful for treating inflammatory and degenerative diseases mediated by	
XX	TNF -	
PT		
XX		
PS	Example 12; Fig 39; 82pp; English.	
XX		
CC	The present invention relates to Tumour Necrosis Factor (TNF) Inhibitor	
CC	(see AAB37676 and AAB37685), which have TNF inhibitory activity. The	
CC	novel TNF inhibitors of the present invention are useful as therapeutic	
CC	agents for inhibiting the activity of TNF and interleukin (IL-1), and	
CC	for treating inflammatory and degenerative diseases mediated by TNF. The	
CC	present invention is the coding sequence for the precursor of 40 kDa TNF	
CC	inhibitor. The 40 kDa TNF inhibitor can inhibit both TNF alpha and beta	
CC	(Lymphotoxin).	
XX		
SQ	Sequence 2394 BP; 484 A; 743 C; 738 G; 428 T; 1 other;	
	Query Match	44.8%; Score 1171; DB 22; Length 2394;
	Best Local Similarity	98.3%; Pred. No. 6.5e-303;
	Matches 1194; Conservative	0; Mismatches 20; Indels 1; Gaps
QY	97 GACCCACCCCATCTTGCTTACAGATTTCTCCCTGGTGGCCATGGAGCCAGGTC	156
DB	1170 GAGGCGCGGCGACAGACCGGAGCTCAGATCTTCCCTGGTGGCCATGGAGCCAGGTC	1229
QY	157 AATGTCACCTGGATGTTGTAAGCTCTGTAGACACTTGACACACGCTCAACAGTCTCTCC	216
DB	1230 AATGTCACCTGGATGTTGTAAGCTCTGTAGACACTTGACACACGCTCAACAGTCTCTCC	1289
QY	217 CAAGCCAGCTCCACATGGAGACACACATTCACAGCCCTCGGAGTCCCGAAGACAG	276
DB	1290 CAAGCCAGCTCCACATGGAGACACACATTCACAGCCCTCGGAGTCCCGAAGACAG	1349
QY	277 GAGGTCCTCTTCTCCAAAGAGATGTCCCTTGGTCACAGCTGGACACCCAGACACC	336
DB	1350 GAGGTCCTCTTCTCCAAAGAGATGTCCCTTGGTCACAGCTGGACACCCAGACACC	1409
QY	337 CTGCTGGGGAGACCGAAGAGAGAGCCCTTGCCCTTGAAGTCCCTGANTGCTGGATGAG	396
DB	1410 CTGCTGGGGAGACCGAAGAGAGAGCCCTTGCCCTTGAAGTCCCTGANTGCTGGATGAG	1469
QY	397 CCCAGTTAACCAAGCCGGGTGTGGCTGTGTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG	456
DB	1470 CCCAGTTAACCAAGCCGGGTGTGGCTGTGTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG	1529
QY	457 ATGACCCCTGCAAGAGGGGCGCTGGTCTTCCCAAGGCCCCCAGACACTAGACACTGAGGCTCT	516
DB	1530 ATGACCCCTGCAAGAGGGGCGCTGGTCTTCCCAAGGCCCCCAGACACTAGACACTGAGGCTCT	1589
QY	517 TTTGCGGCGCAAGTTCCTAGTGCCTCTCACAGCGCGAGGCTCCCTTGACCTGGACAGCC	576
DB	1590 TTTGCGGCGCAAGTTCCTAGTGCCTCTCACAGCGCGAGGCTCCCTTGACCTGGACAGCC	1649
QY	577 AAGAGCAGAGGACACCGAGTTGGGAAAGCCTCTGCTGCATAGTGTGTCCCTCTCGAAG	636
DB	1650 AAGAGCAGAGGACACCGAGTTGGGAAAGCCTCTGCTGCATAGTGTGTCCCTCTCGAAG	1709
QY	637 GCTGGCTGGGCAATGAGCTTGGGGCAATGGTGGGGCAAGTCCCTGACTCTCTGTGACCTG	696
DB	1710 GCTGGCTGGGCAATGAGCTTGGGGCAATGGTGGGGCAAGTCCCTGACTCTCTGTGACCTG	

subject to a pathogen or sterile inflammatory disease using the gene expression profile.

CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 CC particularly in conditions in which both TNF and IL-1 play a causative
 CC role. They may be used to treat cachexia, rheumatoid arthritis,
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
 CC cerebral malaria, allograft and xenograft rejection in graft verses
 CC host disease, sepsis, septic shock, inflammation, allergies and
 CC autoimmune dysfunctions.

SQ Sequence 1641 BP; 328 A; 544 C; 502 G; 267 T; 0 other:

Query Match 17.3% Score 453; DB 14; Length 1641;

Best Local Similarity 96.9%; Pred. No. 8.1e-111;

Matches 462; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 97 GACCCCAACCCATCTTGTCTTACGATTCCTTCCCTGTGTGGCCATGGAGCCAGATC 156
 DB 1165 GAGGCCGGGGCCAGCACCGGAGCTCAGATTTCTCCCTGTGTGGCCATGGAGCCAGATC 1224
 OY 157 AATGTACCTGATGCTGAACGCTGTACAGCTGTGACACAGCTCAGAGTCTCTCC 216
 DB 1225 AATGTACCTGATGCTGAACGCTGTGTAGCAGCTGTGACACAGCTCAGAGTCTCTCC 1284
 OY 217 CAAGCCAGCTCCACAAATGGAGACAGATTCAGCCCTCGAGATCCCGGAAGACGAG 276
 DB 1285 CAAGCCAGCTCCACAAATGGAGACAGATTCAGCCCTCGAGATCCCGGAAGACGAG 1344
 OY 277 CAGGTCCCTTCTCCAGAGAGATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 336
 DB 1345 CAGGTCCCTTCTCCAGAGAGATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 1404
 OY 337 CTGCTGGGAGACACCAAGAGAGCCCTTGGGCTGCTGATGCTGGATGTGAAG 396
 DB 1405 CTGCTGGGAGACACCAAGAGAGCCCTTGGGCTGCTGATGCTGGATGTGAAG 1464
 OY 397 CCCAGTTAACCGCCGGGTGTGTGCTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG 456
 DB 1465 CCCAGTTAACCGCCGGGTGTGTGCTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG 1524
 OY 457 ATGACCCCTCGAAGGGCCCTGTCTTCAGGCCCCCACTAGAGACTGTAGGCTCT 516
 DB 1525 ATGACCCCTCGAAGGGCCCTGTCTTCAGGCCCCCACTAGAGACTGTAGGCTCT 1584
 OY 517 TTCTGGGCCAAGTCTCTAGTGCCTTCAGAGCCGAGCCCTCTGAGACTCTCAG 573
 DB 1585 TTCTGGGCCAAGTCTCTAGTGCCTTCAGAGCCGAGCCCTCTGAGACTCTCAG 1641

RESULT 15

AA045224
 ID AA045224 standard; cDNA: 1641 BP.

AC AA045224:

DT 07-OCT-1994 (first entry)

DE Sequence encoding human tumour necrosis factor receptor type I
 (TNFR1).

DE Tumour necrosis factor receptor; type I; TNFR1: arthritis therapy; ss.

KW Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide 154..1470
 FT sig_peptide 88..153
 FT /*tag= a
 FT /*tag= b

XX MO9406476-A.

XX 31-MAR-1994.

PF 14-SEP-1993; 93MO-US08666.

XX 15-SEP-1992; 92US-0946236.
 PR (IMV) IMMUNEX CORP.
 PA
 XX
 PI Jacobs CA, Smith CA;
 XX
 DR WPI: 1994-118172/14.
 DR P-PSDB: AAR51002.
 PT Treating TNF mediated inflammatory diseases with TNF antagonist -
 PT esp. soluble form of TNF receptor, opt as fusion protein with
 PT human immunoglobulin Fc region, esp. for treating arthritis
 XX
 PS Disclosure: Page 28-30; 47pp; English.

AA045224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
 cell line WI-26 VA4. The mature full-length TNFR1 is a glycoprotein
 having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
 CC TNFR1 was described in Smith et al., Science 248:1019,1990. Clone 1
 CC is contained in expression vector pCAV/Not-TNFR (ATCC 68088). The
 CC preferred TNFRs of the present invention are soluble forms of TNFR1
 CC and TNFR1 having at least 20 AAs. Soluble TNFR constructs are
 CC devoid of a transmembrane region but retain the ability to bind TNF.
 CC Examples of soluble TNFRs are hTNFR1delta235, hTNFR1delta165 and
 CC hTNFR1delta163 which encode respectively AAs 1-235, 1-185 and 1-163
 CC of AAR51002. An equivalent soluble TNFR is hTNFR1delta163 wherein x
 CC is selected from any one of AAs 163-235 of AAR51002.

SQ Sequence 1641 BP; 328 A; 526 C; 520 G; 267 T; 0 other:

Query Match 17.3% Score 453; DB 15; Length 1641;

Best Local Similarity 96.9%; Pred. No. 8.1e-111;

Matches 462; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 97 GACCCCAACCCATCTTGTCTTACGATTCCTTCCCTGTGTGGCCATGGAGCCAGATC 156
 DB 1165 GAGGCCGGGGCCAGCACCGGAGCTCAGATTTCTCCCTGTGTGGCCATGGAGCCAGATC 1224
 OY 157 AATGTACCTGATGCTGAACGCTGTGTAGCAGCTGTGACACAGCTCAGAGTCTCTCC 216
 DB 1225 AATGTACCTGATGCTGAACGCTGTGTAGCAGCTGTGACACAGCTCAGAGTCTCTCC 1284
 OY 217 CAAGCCAGCTCCACAAATGGAGACAGATTCAGCCCTCGAGATCCCGGAAGACGAG 276
 DB 1285 CAAGCCAGCTCCACAAATGGAGACAGATTCAGCCCTCGAGATCCCGGAAGACGAG 1344
 OY 277 CAGGTCCCTTCTCCAGAGAGATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 336
 DB 1345 CAGGTCCCTTCTCCAGAGAGATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 1404
 OY 337 CTGCTGGGAGACACCAAGAGAGCCCTTGGGCTGCTGATGCTGGATGTGAAG 396
 DB 1405 CTGCTGGGAGACACCAAGAGAGCCCTTGGGCTGCTGATGCTGGATGTGAAG 1464
 OY 397 CCCAGTTAACCGCCGGGTGTGTGCTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG 456
 DB 1465 CCCAGTTAACCGCCGGGTGTGTGCTGTAGCCAAAGTGGGCTGAGCCCTGGCAGG 1524
 OY 457 ATGACCCCTCGAAGGGCCCTGTCTTCAGGCCCCCACTAGAGACTGTAGGCTCT 516
 DB 1525 ATGACCCCTCGAAGGGCCCTGTCTTCAGGCCCCCACTAGAGACTGTAGGCTCT 1584
 OY 517 TTCTGGGCCAAGTCTCTAGTGCCTTCAGAGCCGAGCCCTCTGAGACTCTCAG 573
 DB 1585 TTCTGGGCCAAGTCTCTAGTGCCTTCAGAGCCGAGCCCTCTGAGACTCTCAG 1641

Search completed: December 5, 2002, 23:29:22
 Job time: 723.284 secs

697 CCCCCCAGCTGCACCTGCCAGCCTGGCTTCTGGAGCCCTTGGGTTTGTGTTG 756

FEATURES	Location/Qualifiers
source	1..1029

Source

721 GCCTGCCTGCACTGACCTGCACCTGTACTCAANNAGAGCTGANNCGAGATCATTNGAGCC 780

Y 1729 CTTCAATTCCGTGGCCCCAAG - GGGCTGCCCTGCCACTTTGGTACATGGCCAGTGTGAT 1787

[illegible]

AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC,
JOURNAL	unpublished (1999)
COMMENT	Contact: Robert Strussberg, Ph.D

Email: cgapds-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Abencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: LLCM202 row: d column: 12
High quality sequence step: 657.

FEATURES	Location/Qualifiers
source	1.,.1022

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480027"
/clone_lib="NH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pORB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACAGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC library."

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BASE COUNT	231 a	303 c	260 g	228 t
ORIGIN				

Query Match	Score	DB	Length
Best local similarity	811	14	1022

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Best Local Similarity  94.5%;  Pred. No. 4.5e-122;
Matches  919;  Conservative  0;  Mismatches  40;  Indels  14;  Gaps  7.

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749 TTTGTTTGTGTTGTTGTTGTTGTTTCCTCCCGCTGGGCTCTG-CCCAAGCTCTGGCTTCC 800

Db 1 TTTGTTGTTGTTGTTGTTCTCCCCGSGCTCGCCCCAGCTCGGCTTC 60

808 AGAAACCCAGCATCCTTTCTGCGAGAGGGGCTTCTGGAGAGAGGCGATGCTGCTGA 86

D6
61 AGAAACCCAGCATTCTTGGAGAGGCGCTTCGCCAGCCATGCACCACTG

[illegible]

121 CCGAGGCTGGTGGATGGGTCCGGC 92

121 GTCACCCATGAAGACACAGCAGTGCCTTCAGCCTGAGGCTGAGACTGCGGGATGCTCTGC 18

928 GGCCTCTGTGTAGGGAGGAGGTGGCAGCCCTGTATGGGAACGGGGTCCCTTCAAGTTACCTCA 98

Db 181 GGCCTGTGCAGGAGGAGGTGGCAGCCCTCTAGGGACGGGGCTTCAAGTTACTTCA 24

988 GGAGGCTTGGAAAGCATCACCCTCAGGCCAGGTTCAGTGCGTCAAGCCTATGATCCACGA 10

Db 241 GGAGGCTTGGAAAGCATCACCCTCAGGCCAGTGCAGTGGCTCAGCCCTATGATCCGACA 30

OY 1048 CTTTGGAGCCTGAGGCGGTGATCACCTGAGGTTAGGATTGAGACCAAGCTGGCCA 11

D6
301 CTTTGGAGGCTTAGCCCGCCTGCATCAACGCCGCCCCCCC
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Ov

1108 ACATGCGTAAACGGCAAGCTGCATTCTTTTCCTCCTA 36

-CCGCCCATGACCCTGTGTAATCCCCTTGATGGAAGGCTGCTG

2100 ACGGCGTGGGACATCTACCAAAACAGAAATTAGCCGGGGCTGTGGGGGCA 11
261 |||||

361 ACATGGTAAACCCCATCTCTACTAAATAACAGAAATTACCGGGCGGTGTGGCGGGCA 42

1168 CCTATTAGTCCACGCTACTCAGAAAGCCTGAGGCTGGGAATCGTTTGAACCCGGGAAGCGG 12

Db 421 CCTATAGTCCACGCTACTCAGAACCTGAGGCTGGGAATCTTTGAAACCCGGGAGCGG 48

1228 AGGTTGCAGGGAGCCGAGATCACGCCACTGCACTCCAGCCTGGGGCAGACAGCCGAGAGTC 1235

Db 481 AGGTTGCAGGAGCCGAGATCACGCCACTGCACCTGGGGCGACAGAGCGAGCTC 54

QY 1288 TGTCTCAAAAGAAAAACGACCCGCTCCAAATGCTAACCTGTCCTTTGTACCA 13

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Db 541 TGTCTCAAAAG-AAAAAAAAAAGCACCGCTCCAAATGCTACTTGTCTTTTGTACCA 599
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600 TGGGTGTGAAGTCACATGCCCGAGAGGCCGAGGCCACCATATTCAGTGTGGC 659
1407 CTGGGCAAGTAAGCAGCTTCTAAGTAATTCGCAATTTTAAAGTAAGTACAC 1466
660 CTGGGCAAGTAAGCAGCTTCTAAGTAATTCGCAATTTTAAAGTAAGTACAC 719
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780 TGGCAATTCGACCTTCGCGC-TTCACTCCGCTGTGCTGAGAGCCGCGCTCTT 839
1586 GCTGTCTTGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1641
840 GCTGTCTTGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 899
1642 AGTCTCTTGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1695
900 AGTCTCTTGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 959
1696 CAGAGGGGTGGGT 1708
960 CCAAAAGGGGT 972

RESULT 5
B0052282/c 1053 bp mRNA linear EST 29-MAR-2002
LOCUS B0052282
DEFINITION AGENCOURT_6868457 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:593511
5', mRNA sequence.
ACCESSION B0052282
VERSION B0052282.1 GI:19811622
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1053)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM2118 row: c column: 16
High quality sequence stop: 649.
Location/Qualifiers
1..1053
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:593511"
/clone_lib="NIH_MGC_106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: blood; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

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BASE COUNT 216 a 328 c 297 g 212 t
ORIGIN
Query Match 31.0%; Score 810.8; DB 14; Length 1053;
Best Local Similarity 92.0%; Pred. No. 4,8e-122;
Matches 957; Conservative 0; Mismatches 67; Indels 16; Gaps 9;

Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library.

287 TCTCCAGGAGGAGATGCTTGGTGTGCTACAGCTGTGAGAGCCAGAGCC-TCG 340
1053 TCCCAAGGGGGGAGAGCCCTTGGGTCCCAAGCTGTGAGAGCCAGCCCTGTGG 994
341 TGGGAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 397
993 GAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 934
398 CCAGTTAACAGAG-CCGGGTGGGCTGTGTGTGAGAGAGAGAGAGAGAGAG 456
933 CCAGTTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
457 ATGACCTGCG-AAGGGCCCTGTGCTTCCAGAGCCCTTCCAGAGAGAGAG 513
873 AAGAGCCCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
514 TCTTTCTGGG-CCAAGTTCTGTAGTGGCTTCACAGAGAGAGAGAGAGAG 572
813 TCTTTCTGGG-CCAAGTTCTGTAGTGGCTTCACAGAGAGAGAGAGAGAG 754
573 GG-CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
753 GGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 694
632 GGAAGGCTGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691
693 GGAAGGCTGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 634
692 ACCGCCCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
633 ACCGCCCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 574
752 GTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 751
573 GTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 810
811 AAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 514
513 AAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 454
871 ACCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
453 ACCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 394
931 TCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
993 TCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
991 GCGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
333 GCGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 274
1051 TGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
273 TGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 214
1111 TGGTAAAGCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1170
213 TGGTAAAGCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 154
1171 ATAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
153 ATAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 94

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Qy	1231	TTTGAGGAGCCGAGATCAGCCACTGCATCCAGCTGGGGACAGAGCCGAGATCTGT	1230
Db	93	TTTGAGGAGCCGAGATCAGCCACTGCATCCAGCTGGGGACAGAGCCGAGATCTGT	34
Qy	1291	CTCAAAAGAAAAAAAAA	1310
Db	33	CTCAAAAGAAAAAAAAA	14

RESULT 6	
B0690571	
LOCUS	B0690571
DEFINITION	B0690571 945 bp MRNA linear EST 15-JUL-2002
	AGENCOUNT 8342072 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248991
	5' , mRNA sequence.

VERSION	BO690571.1	GI:21815867
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
TITLE	1 (bases 1 to 945)	
JOURNAL	NIH-MGC http://mgc.ncl.nih.gov/ .	
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)	
	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LNCM2389 row: 1 column: 16
High quality sequence count: 588.
Location/Qualifiers
1..945
FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6248991"
/clone_1ib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pORF7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by Oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using
the following 5' adaptor: GCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

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		30.5%	Score 797.2;	DB 14;	Length 945;
Query Match					
Host Local Similarity		97.3%;	Pred. No. 8.1e-120;		
Matches	853; Conservative	0; Mismatches	19; Indels	5; Gaps	4;
QY	1659 CTCTACTCCTACCTAGCCCTGAGCCCTTCCTCTCCCCAGAGGGGTGGTTCTCTTCCC				1718
Db	1 CTTCTATCTCCCTACTAGCTAGGCCCTCTCTCTCCCCAAGAGGGGTGGTTCTCTTCCC				60
QY	1719 CACTCCCAACCTTCATTCTCGGGCCCCAAAGGGGTGCCTCCGCACTTGGTGACATGGC				1778
Db	61 CACTCCCAACCTTCATTCTCGGGCCCCAAAGGGGTGCCTCCGCACTTGGTGACATGGC				120
QY	1779 CAGTGGATGCCAATGGCACTTGTGTGTGGCCTCTGTGTTCGCTGTGCTGGGTGTGG				1838
Db	121 CAGTGTGATCCCAATGGCACTG				180
QY	1839 TACCCAAGTGGGTGAATGTAATGGCTTCCTTGAAACCACCTGAACCTGGATTCCTCCC				1898

Db	181	TACCCAAAGTCGGTAACTTGAATGATGCGCTTGTGAAAGCCACTGAAAGCTGGCATTTCTCC	240
Qy	1899	CATTAGAGTCAGCCCTTCCCTCCACAGGGCCAGAGGCCCTTGCAGAGGGGAAACCAAGTGTAG	1958
Db	241	CATTAGAGTCAGCCCTTCCCTCCACAGGGCCAGAGGCCCTTGCAGAGGGGAAACCAAGTGTAG	300
Qy	1959	CGTTGCCCGGATTTCTGGGAGCAAGCGTTGAGGGGCTCTCTGGAAAGGCTCAGTCTCAGG	2018
Db	301	CGTTGCCCGGATTTCTGGGAGCAAGCGTTGAGGGGCTCTCTGGAAAGGCTCAGTCTCAGG	360
Qy	2019	AGCATGGGGATTAAGAGAAAGGCATAAATTTGCTTAGCAGACAGAGGGCCAGGGTGTATAA	2078
Db	361	AGCATGGGGATTAAGAGAAAGGCATAAATTTGCTTAGCAGACAGAGGGCCAGGGTGTATAA	420
Qy	2079	TTTGTTGTAATAATTTCCACTGCATCTTGACCTTTGGCAGCTGACACTATTGAGGCTGGAGAGC	2138
Db	421	TTTGTTGTAATAATTTCCACTGCATCTTGACCTTTGGCAGCTGACACTATTGAGGCTGGAGAGC	480
Qy	2139	CCAGCCATTACCATGAGACAAAGAGGTTTTTCCACCCTGGGAATTCAGATGTCAGACTGG	2198
Db	481	CCAGCCATTACCATGAGACAAAGAGGTTTTTCCACCCTGGGAATTCAGATGTCAGACTGG	540
Qy	2199	CTGGCTGCAGTGAACGTGCACCTGTACTCAGAGGCTGAGGGGAGAGATCAGTGAAGCCACG	2258
Db	541	CTGGCTGCAGTGAACGTGCACCTGTACTCAGAGGCTGAGGGGAGAGATCAGTGAAGCCACG	600
Qy	2259	GAGTTTGAAGCTGAGAGGAGCTATGATGGCGGCACCTACACATCCAGCCCTGAGCAACAGACT	2318
Db	601	GAGTTTGAAGCTGAGAGGAGCTATGATGGCGGCACCTACACATCCAGCCCTGAGCAACAGACT	660
Qy	2319	GAGACCCCTGTCTCTTTAAAGAAAAAAAAGTCAGACTGCTGGGAGCTGGCCAGGTTTCTGCC	2378
Db	661	GAGACCCCTGTCTCTTTAAAG - AAAAAAAAAGTCAGACTGCTGGGAGCTGGCCAGGTTTCTGCC	719
Qy	2379	CACATTGAGACCCACATGAGGACATGATGAGAGCGGACACTG - CCCCCTGGTGGACAGTCTCT -	2436
Db	720	CACATTGAGACCCACATGAGGACATGATGAGAGCGGACACTG - CCCCCTGGTGGACAGTCTCT	779
Qy	2437	GGGGAAGCTCAGGCTTCCCTTGGCATCAGAGGGCAGAGCCGGGAGG - -GCATGAAATTTGG	2494
Db	780	GGGGAAGCTCAGGCTTCCCTTGGCATCAGAGGGCAGAGCCGGGAAAGCAATGAAATTTGG	839
Qy	2449	AGACTGTGGGGCTTGGTTCCCTTTGTGTGTGTGTG 2531	
Db	840	AGACTGTGTGGGGCTTGGTTCCCTTTGTGTGTGTGTG 876	

RESULT	7				
LOCUS	B1838021				
DEFINITION	B1838021	771 bp	mRNA	linear	EST 04-OCT-2001
ACCESSION	G03083859F1 NIH_MGC_120	Homo sapiens	cDNA clone	IMAGE:5222896 5'	
VERSION	B1838021				
KEYWORDS	B1838021.1	GI:15949571			
SOURCE	EST.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
JOURNAL	1 (bases 1 to 771)				
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .				
	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-remail.nih.gov				
	Tissue Procurement: Life Technologies, Inc.				
	cDNA Library Preparation: Life Technologies, Inc.				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Place: LLNL1560	Row: j	Column: 17		

non-activated adult donors. Library is oligo-dT primed and directionally cloned (copy site is destroyed upon cloning). Average insert size 1.7 kb. Insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH-MGC Library."

BASE COUNT 176 a 243 c 177 g 163 t

ORIGIN

Query Match 25.8%; Score 675; DB 13; Length 759;

Best Local Similarity 97.1%; Pred. No. 5.6e-100;

Matches 741; Conservative 0; Mismatches 15; Indels 7; Gaps 5;

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Db 1 CGGGACACTATATCCAGCTACTGAGAAAGCCGAGGCGGGAATCCGTGAACCCGGG 60

QY 1222 AAGCGAGCTTGCGAGGAGCCGAGATCAGCCACTGCATCCAGCCTGGGAGAGAGCG 1281

Db 61 AAGCGAGCTTGCGAGGAGCCGAGATCAGCCACTGCATCCAGCCTGGGAGAGAGCG 120

QY 1282 AGAGTCGTCTCAAAAGAAAAAAGCAAGCCGCTCCAAATGCTAACTTGTCTTTT 1341

Db 121 AGAGTCGTCTCAAAAG--AAAAAAGAGCAAGCCGCTCCAAATGCTAACTTGTCTTTT 178

QY 1342 GTACCATGTGTGAAGTGAAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1401

Db 179 GTACCATGTGTGAAGTGAAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 238

QY 1402 GTGGGCTGGGCAAGATTAAGGCACTTCTAATGAAATGTGCCAA-TTTTTTAAAAAGTA 1460

Db 239 GTGGGCTGGGCAAGATTAAGGCACTTCTAATGAAATGTGCCAA-TTTTTTAAAAAGTA 298

QY 1461 AGTACCACTAGAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1520

Db 299 AGTACCACTAGAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 358

QY 1521 CCCACTGGCATTTGACCCCTCCGCTTCACTCCGCTGCTGCTGCTGCTGCTGCTGCT 1580

Db 359 CCCACTGGCATTTGACCCCTCCGCTTCACTCCGCTGCTGCTGCTGCTGCTGCTGCT 418

QY 1581 TCCCTGCTGCTTACGACACACATCTCTTTCAGGGGATTTGAGGAAGTGAAGTACT 1640

Db 419 TCCCTGCTGCTTACGACACACATCTCTTTCAGGGGATTTGAGGAAGTGAAGTACT 478

QY 1641 GAGTCTCTGTAGCACTCTCTACTCTACCTAGAGCTAGAGCCCTCTCTCTCCCGAG 1700

Db 479 GAGTCTCTGTAGCACTCTCTACTCTACCTAGAGCTAGAGCCCTCTCTCTCCCGAG 538

QY 1701 GAGTCTCTGTAGCACTCTCTACTCTACCTAGAGCTAGAGCCCTCTCTCTCCCGAG 1760

Db 539 GAGTCTCTGTAGCACTCTCTACTCTACCTAGAGCTAGAGCCCTCTCTCTCCCGAG 595

QY 1761 GCCACTTTGTGATAGGCACTGTGATGCCAAGTGCAGT-CTTGTGTGCTGCTGTGTG 1819

Db 596 GCCACTTTGTGATAGGCACTGTGATGCCAAGTGCAGT-CTTGTGTGCTGCTGTGTG 655

QY 1820 TCCGCTGCTGCTGTGATGAGCAAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1879

Db 656 TCCGCTGCTGCTGTGATGAGCAAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 715

QY 1880 TGAAGCTGGATCTCTCCCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1922

Db 716 TGAAGCTGGATCTCTCCCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 758

RESULT 12

LOCUS BG746069

DEFINITION 60273532T1 NIH_MGC_113 Homo sapiens cdna clone IMAGE:4850143 3',

ACCESSION BG746069

958 bp mRNA linear EST 15-MAY-2001

VERSION BG746069.1 GI:14056722

KEYWORDS EST

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 958)

AUTHORS NIH-MGC

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM1690 row: 0 column: 08

High quality sequence start: 3

High quality sequence stop: 791.

Location/Qualifiers

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/lab_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pORF7; Site: 1; XhoI; Site: 2;

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGAGG(6). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH-MGC Library."

BASE COUNT 220 a 305 c 227 g 206 t

ORIGIN

Query Match 24.9%; Score 650.6; DB 12; Length 958;

Best Local Similarity 89.0%; Pred. No. 4.3e-96;

Matches 852; Conservative 0; Mismatches 84; Indels 21; Gaps 13;

QY 1617 GAATTCGAGAACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1675

Db 957 GAATTCGAGAACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 898

QY 1676 CCTAGACCCCTCTCTCT--CCGCCAGAGGGGTGGTCTCTCTCTCTCTCTCTCTCTCA 1734

Db 897 CCTAGACCCCTCA 838

QY 1735 TTCTGAGGCGCCCAAGCGGCTG---CCCTGCCACTTTGGTATGATGATGATGATGAT 1790

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QY 1791 AAGTCCAGTC--TTGTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1846

Db 777 AAGTCCAGTC--TTGTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 718

QY 1847 GTCCGT--AAGTGAATGCTGCTGTGAAGCACTGAAGCTGGATTCCTCCCATTTGA 1905

Db 717 GTCCGT--AAGTGAATGCTGCTGTGAAGCACTGAAGCTGGATTCCTCCCATTTGA 658

QY 1906 GTCCGTCTC---CCCTCCAGGGGCGCCCTGCAAGGGGAAACAGTGTAGCTTT 1962

Db 657 GTCCGTCTC---CCCTCCAGGGGCGCCCTGCAAGGGGAAACAGTGTAGCTTT 598

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Oy 2200 TGGCTG-CAGTGAAGCTGACCTTACTCAGAGAGCTGAGGGAGAGTCACTGGAGCCGAG 2258
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Oy 2259 GAGTT-TGAGGCTGACAGGAGCTATGATGGCGCAGTCACTGACCTGAGCAAGAGAG 2317
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KEYWORDS B0632819.1 GI:21684337
SOURCE EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 655)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
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Hillier,L., Merra,M., Pape,D., Wylie,T., Martin,J., Blistein,A.,
Schmitt,A., Theising,B., Riltter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarelisvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: 1128603.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
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Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
BASE COUNT 122 a 179 c 207 g 147 t
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Query Match 24.1%; Score 629.8; DB: 14; Length 655;
Best Local Similarity 99.5%; Pred. No. 1,3e-92;
Matches 642; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Oy 683 CTCTCTGTGACCTGCCCGCCAGCTGACCTGCCAGCTTGGCTTGGAGCCCTTGGGT 742
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Db 251 GCTTCAGTACCCATGAGAGAGAGAGAGAGTGTTCAGCTTGAAGCTGAGAGTGGGATG 310
Oy 922 TCCCTGGGCTGTGTGTAGAGAGAGAGTGGAGGCTTGTAGAGAGGAGGCTTCAAGTT 981
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Oy 982 AGCTAGAGAGCTTGTGGAAGCATCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1041
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RESULT 14
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DEFINITION HPM1-1841AF. HPM1 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE440065
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TITLE        1 (bases 1 to 672)
AUTHORS      Gonzalez, P., Epstein, D.L. and Borras, T.
JOURNAL      Characterization of gene expression in human trabecular meshwork
              using single-pass sequencing of 1060 clones
COMMENT      Invest. Ophthalmol. Vis. Sci., (2000) In press
              Contact: Pedro Gonzalez
              Department of Ophthalmology
              Duke University
              Duke Eye Center, Erwin Rd, Box 3802, Durham, NC 27710-3802, USA
              Tel: 919 681 4085
              Fax: 919 684 8983
              Email: pedro.gonzalez@duke.edu.

FEATURES
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Qy 1449 TTTAAAAAGTAAGTACACTCAGGCCAACAAGCAAGCAAAAGCCAAACTCTGCAGC 1508
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VERSION     A1813532.1 GI:5424738
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AUTHORS      1 (bases 1 to 733)
TITLE        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Life Technologies catalog #: 11547-015
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
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BASE COUNT   162 a 211 c 192 g 164 t 4 others

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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2493	95.4	3683	US-09-844-634-3	Sequence 3, Appl1
3	1034	39.6	2224	US-08-477-347-2	Sequence 2, Appl1
4	1034	39.6	2224	US-08-476-862-1	Sequence 1, Appl1
5	453	17.3	1641	US-08-385-229-1	Sequence 1, Appl1
6	453	17.3	1641	US-08-650-000-1	Sequence 1, Appl1
7	453	17.3	1641	5395760-1	Patent No. 5395760
8	284.2	10.9	519	US-09-844-634-19	Sequence 19, Appl
9	234.4	9.0	29629	US-09-729-995-3	Sequence 3, Appl1
10	233.8	8.9	81001	US-09-750-580-1	Sequence 15, Appl
11	232.8	8.9	17327	US-07-906-871-15	Sequence 15, Appl
12	231.8	8.9	631	US-09-385-982-354	Sequence 354, App
13	231.8	8.9	15977	US-09-608-285A-59	Sequence 59, Appl
14	231.8	8.9	62804	US-09-800-960-3	Sequence 3, Appl1
15	231.4	8.9	14581	US-08-520-373D-4	Sequence 4, Appl1
16	231.4	8.9	22481	US-08-367-841A-43	Sequence 43, Appl
17	231.4	8.9	22481	PCT-US95-07201-43	Sequence 43, Appl
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19	231.2	8.8	14747	US-09-608-285A-12	Sequence 42, Appl
20	230.8	8.8	55827	US-09-813-133A-3	Sequence 3, Appl1
21	228.8	8.8	45346	US-09-146-053-6	Sequence 6, Appl1
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23	228.8	8.8	4823	US-08-484-257-20	Sequence 20, Appl
24	228.8	8.8	4823	US-08-999-927-5	Sequence 5, Appl1
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C 33	226.8	8.7	282	1	US-08-133-629-8	Sequence 8, Appl1
C 34	226.6	8.7	50000	4	US-09-146-053-3	Sequence 3, Appl1
C 35	226.6	8.7	11282	4	US-09-754-230-3	Sequence 3, Appl1
C 36	226.4	8.7	8453	4	US-09-167-681-45	Sequence 45, Appl
C 37	226.2	8.7	5232	3	US-08-212-971-3	Sequence 3, Appl1
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C 42	225.6	8.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
C 43	225.6	8.6	246240	2	US-08-724-394A-22	Sequence 22, Appl
C 44	225.4	8.6	98844	4	US-09-791-211-10	Sequence 10, Appl
C 45	224.8	8.6	20674	4	US-09-641-638-651	Sequence 651, App

ALIGNMENTS

RESULT 1
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; Sequence 17, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRE
; FILE REFERENCE: RFS-0216
; CURRENT APPLICATION NUMBER: US/09/844,634
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 17
; LENGTH: 15602
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-844-634-17

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QY	481	CTTTCACAGGCCCCCACCACACTAGACACTGTAGAGGCTTTTCTGGGGCCAAAGTTCCTCTATGTGC	540
Db	11084	CTTTCACAGGCCCCCACCACACTAGACACTGTAGAGGCTTTTCTGGGGCCAAAGTTCCTCTATGTGC	11143
QY	541	CTTTCACAGGCCCCCACCACACTGTAGAGGCTTTTCTGGGGCCAAAGTTCCTCTATGTGC	600
Db	11144	CTTTCACAGGCCCCCACCACACTGTAGAGGCTTTTCTGGGGCCAAAGTTCCTCTATGTGC	11203
QY	601	AAAGCCCTCTGCTCCCAATGGTGTGTCTCTCTCGGAAGGCTGGCTGGGCATGTGACGTTCCGG	660
Db	11204	AAAGCCCTCTGCTCCCAATGGTGTGTCTCTCTCGGAAGGCTGGCTGGGCATGTGACGTTCCGG	11263
QY	661	GCATGCTGGGGGCAAGTCCCTGACATCTGTGTGACCTTCCCGCCAGCTCACCTGCGCAC	720
Db	11264	GCATGCTGGGGGCAAGTCCCTGACATCTGTGTGACCTTCCCGCCAGCTCACCTGCGCAC	11323
QY	721	CTGGCTTCTGGAGCCCTTGAGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Db	11324	CTGGCTTCTGGAGCCCTTGAGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	11383
QY	781	CTGTGGCTCTG-CGCCAGCTCTGGCTTCCAGAAACCCAGCATCTTTTCTGACAGGGG	839
Db	11384	CTGTGGCTCTGCGCCCCAGCTCTGGCTTCCAGAAACCCAGCATCTTTTCTGACAGGGG	11443
QY	840	CTTTTCTGGAGAGAGGAGGATGCTGTCTGTGATCACCCTAGAGACAGACAGTCTTCAGCC	899
Db	11444	CTTTTCTGGAGAGAGGAGGATGCTGTCTGTGATCACCCTAGAGACAGACAGTCTTCAGCC	11503
QY	900	TCAGCTCTGAGACTGCGGAGTGTGTCTCGGGGGCTGTGTGTGGAGAGAGGTGGAGCCGT	959
Db	11504	TCAGCTCTGAGACTGCGGAGTGTGTCTCGGGGGCTGTGTGTGGAGAGAGGTGGAGCCGT	11563
QY	960	AGGGAAGGGGGTCTTCAAGTTAGCTCAGAGAGGCTTGGAAAGCATCACCTCAGGCCAGGT	1019
Db	11564	AGGGAAGGGGGTCTTCAAGTTAGCTCAGAGAGGCTTGGAAAGCATCACCTCAGGCCAGGT	11623
QY	1020	GCAGTGGCTCAGAGCCATATATCCCGAGCACTTTGGGAGGCTGAGCGGGGTGCATCCTGA	1079
Db	11624	GCAGTGGCTCAGAGCCATATATCCCGAGCACTTTGGGAGGCTGAGCGGGGTGCATCCTGA	11683
QY	1080	GGTTAGGAGTTTGAGAGCCAGCCTTGCCCAACATGTATAAACCCCATCTCTACTAAAAATAC	1139
Db	11684	GGTTAGGAGTTTGAGAGCCAGCCTTGCCCAACATGTATAAACCCCATCTCTACTAAAAATAC	11743
QY	1140	ACAAATTTAGCCGGGCTGTGTGGCGGCACTATAGTCCAGCTACTCGAAAGCTTGAGGC	1199
Db	11744	ACAAATTTAGCCGGGCTGTGTGGCGGCACTATAGTCCAGCTACTCGAAAGCTTGAGGC	11803
QY	1200	TGGGAAATTCGTTTGAACCCGGGGAACGGGAGTGTGAGGAGCCCGAGTACAGGCCACTGCA	1259
Db	11804	TGGGAAATTCGTTTGAACCCGGGGAACGGGAGTGTGAGGAGCCCGAGTACAGGCCACTGCA	11863
QY	1260	CTTCAGCCTGGGCGACAGAGCGAGAGTCTGTCTCAAAAGAAAAAAGAAAAAGACCGGCT	1319
Db	11864	CTTCAGCCTGGGCGACAGAGCGAGAGTCTGTCTCAAAAGAAAAAAGAAAAAGACCGGCT	11921
QY	1320	CCAAATTCGTAACCTTCTCTTTTGTACCAATGGTGTGAAAGTCAGATGCCAGAGGGCCAG	1379
Db	11922	CCAAATTCGTAACCTTCTCTTTTGTACCAATGGTGTGAAAGTCAGATGCCAGAGGGCCAG	11981
QY	1380	GCAGGCGACCAATTTCACTGCTGTGGCTTGCGCAAGATTAACGACTTTCTAATCTGAATTC	1439
Db	11982	GCAGGCGACCAATTTCACTGCTGTGGCTTGCGCAAGATTAACGACTTTCTAATCTGAATTC	12041
QY	1440	TGCCAAATTTTTTAAAAAAGTAAGTACACATCAGGCCCAACAGCCACCAAGCCCAAC	1499
Db	12042	TGCCAAATTTTTTAAAAAAGTAAGTACACATCAGGCCCAACAGCCACCAAGCCCAAC	12101

QY	1500	TCTGCCAGCCACATCCAAACCCCCACCCTGCATTTGACACCTCCGGCTTCACTCCGGT	1559
Db	12102	TCTGCCAGCCACATCCAAACCCCCACCCTGCATTTGACACCTCCGGCTTCACTCCGGT	1216
QY	1560	GCCTGCAGCCCGCGCCCTCCCTTCTGCTCTCTAGGCCACACATTCCTTTACGGAA	1619
Db	12162	GCCTGCAGCCCGCGCCCTCCCTTCTGCTCTCTAGGCCACACATTCCTTTACGGAA	1222
QY	1620	TTTTCAGGAAGTATGAGATGACTGATGCTCTCTAGCCATCTCTCTACTCTGACGCTA	1679
Db	12222	TTTTCAGGAAGTATGAGATGACTGATGCTCTCTAGCCATCTCTCTACTCTGACGCTA	1228
QY	1680	GACCCCTCCCTCCCGCCCAAGAGGGTGGGTCTCTTCCCACTCCCACTTTCAATTCCT	1739
Db	12282	GACCCCTCCCTCCCGCCCAAGAGGGTGGGTCTCTTCCCACTCCCACTTTCAATTCCT	1234
QY	1740	GGGCCCCCAAGCGGGCTGCCTCTGCACATTTGGTACATGAGCCAGTGTGATCCCAAGCCAG	1799
Db	12342	GGGCCCCCAAGCGGGCTGCCTCTGCACATTTGGTACATGAGCCAGTGTGATCCCAAGCCAG	1240
QY	1800	TCTTGTGCTCGCTCTGTGTTGGCTGTCTGTGGTGTGTGTACCCAAAGTCCGTAAATTGA	1859
Db	12402	TCTTGTGCTCGCTCTGTGTTGGCTGTCTGTGGTGTGTGTACCCAAAGTCCGTAAATTGA	1246
QY	1860	ATGGCCTCCCTTTGAAGCCACTGAAAGCGGGATTTCCCTCCCATTAAGTCACCTTCCCC	1919
Db	12462	ATGGCCTCCCTTTGAAGCCACTGAAAGCGGGATTTCCCTCCCATTAAGTCACCTTCCCC	1252
QY	1920	TCCCAAGGCCCAAGGGCCCTGCCAAGGGGAAACCATGTGTACCTTGGCCGGATTTGGAGG	1979
Db	12522	TCCCAAGGCCCAAGGGCCCTGCCAAGGGGAAACCATGTGTGTACCTTGGCCGGATTTGGAGG	1258
QY	1980	AAGCAGTTGTAGGGGCTCTGTGGAAGGCTACGTCTCAGAGCATGGGATTAAGACAAAG	2039
Db	12582	AAGCAGTTGTAGGGGCTCTGTGGAAGGCTACGTCTCAGAGCATGGGATTAAGACAAAG	1264
QY	2040	GCATGAAATTTCTTACGACAGACGAGGGGAGGGTGAATAATTTGTTGATMAATTTCCACTGCA	2099
Db	12642	GCATGAAATTTCTTACGACAGACGAGGGGAGGGTGAATAATTTGTTGATMAATTTCCACTGCA	1270
QY	2100	CTTGGAGTTGGACACCTGAACATATTGGAGGGTGGAGAGCCCAAGCATTAAGATGGAGACA	2159
Db	12702	CTTGGAGTTGGACACCTGAACATATTGGAGGGTGGAGAGCCCAAGCATTAAGATGGAGACA	1276
QY	2160	AGAAAGGTTTTCCACCCTGTGAATCAAGATGTAGAGTGGTGGCTGCAGTAGACCTGCACC	2219
Db	12762	AGAAAGGTTTTCCACCCTGTGAATCAAGATGTAGAGTGGTGGCTGCAGTAGACCTGCACC	1282
QY	2220	TGTACTCAGAGAGGCTGAGGGGAGAGATCACTGAGCCCAAGGATTTGAGGCTGCACCGAGC	2279
Db	12822	TGTACTCAGAGAGGCTGAGGGGAGAGATCACTGAGCCCAAGGATTTGAGGCTGCACCGAGC	1288
QY	2280	TATATATGCCCCCACTACACTCCAGCCTGTGAGCAAGAGTGTGAGACCCGTCTTTAAAGAA	2339
Db	12882	TATATATGCCCCCACTACACTCCAGCCTGTGAGCAAGAGTGTGAGACCCGTCTTTAAAGAA	1294
QY	2340	AAAAAAGTCAAGACTGCTGGAGCTGCCAGGTTTTCTGCCCAATTGGACCCACATGAGGA	2399
Db	12942	AAAAAAGTCAAGACTGCTGGAGCTGCCAGGTTTTCTGCCCAATTGGACCCACATGAGGA	1300
QY	2400	CATATATGAGACCGACACCTGGCCCCCTGGTGGACAGCTCTGTGGGAAACCTCAGGCTTCTTG	2459
Db	13002	CATATATGAGACCGACACCTGGCCCCCTGGTGGACAGCTCTGTGGGAAACCTCAGGCTTCTTG	1306
QY	2460	CATCACAGGCGACAGCGCGGAAAGCATGAATTTGGAGACTCTGTGGGCGTTTGTTCCCT	2519
Db	13062	CATCACAGGCGACAGCGCGGAAAGCATGAATTTGGAGACTCTGTGGGCGTTTGTTCCCT	1312
QY	2520	TGTGTGTGTGTGTTGATTCGCAAGACAATGAAGTTTGACACTGTATGCTGGAGCGCATTC	2579
Db	13122	TGTGTGTGTGTGTTGATTCGCAAGACAATGAAGTTTGACACTGTATGCTGGAGCGCATTC	1318
QY	2580	TGCTTATCAATAAACCTGTTTTTTTTTAA 2608	

Db 13182 TCGTTATCAATAAACCTGTTGTTTACA 13210

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RESULT 2
US-09-844-634-3
: Sequence 3, Application US/09844634
: Patent NO. 6410324
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSION
: FILE REFERENCE: RFS-0216
: CURRENT APPLICATION NUMBER: US/09/844,634
: CURRENT FILING DATE: 2001-04-27
: NUMBER OF SEQ ID NOS: 174
: SEQ ID NO 3
: LENGTH: 3683
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (90)...(1475)
: US-09-844-634-3

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Query Match	95.48;	Score 2493;	DB 4;	Length 3683;
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Matches 2502; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

OY	97	GACGCCAACCCATTTGGTTAGCAGATTTCTTCCCTGGTGGGCAATGGGACCCAGATC	156
Db	1167	GAGGGCCCGGCGCAGACCGGAGCTCAGATTCTTCCCTGGTGGCAATGGGACCCAGATC	1226
OY	157	AATGTCACCTGCTATGCTAAGCTCTGTAGACACTGTGACCAACGCTCAGTGCCTCC	216
Db	1227	AATGTCACCTGCTATGCTAAGCTCTGTAGACACTGTGACCAACGCTCAGTGCCTCC	1286
OY	217	CAAGCAGCTCCACAAATGGGAGACACAGATTCCAGACCCCTGGAGATCCCCCAAGACAG	276
Db	1287	CAAGCAGCTCCACAAATGGGAGACACAGATTCCAGACCCCTGGAGATCCCCCAAGACAG	1346
OY	277	CAGGTCCTCTTCCAAAGAGAAATGCGCTTTGGGTACACAGCTGGAGACCCAGAGACC	336
Db	1347	CAGGTCCTCTTCCAAAGAGAAATGCGCTTTGGGTACACAGCTGGAGACCCAGAGACC	1406
OY	337	CTGCTGGGGAGCACCGAAGAGAAAGCCCTGCCCTTTGGAGTGCCTGATGCTGGGATGAG	396
Db	1407	CTGCTGGGGAGCACCGAAGAGAAAGCCCTGCCCTTTGGAGTGCCTGATGCTGGGATGAG	1466
OY	397	CCCAATTAAACGAGCGGTTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	456
Db	1467	CCCAATTAAACGAGCGGTTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1526
OY	457	ATGACCTTGCGAAGGGGCCCTGTGTCCTTTCACAGGCCCCACCACTAGGACTTGAAGGCTCT	516
Db	1527	ATGACCTTGCGAAGGGGCCCTGTGTCCTTTCACAGGCCCCACCACTAGGACTTGAAGGCTCT	1586
OY	517	TTTCTGGGCGAAGTTCTCTAGTGCCTTCACAGCGGACGCTGCTCTGACCTCCAGAGCC	576
Db	1587	TTTCTGGGCGAAGTTCTCTAGTGCCTTCACAGCGGACGCTGCTCTGACCTCCAGAGCC	1646
OY	577	AAGAGCAGAGGCACCGAGTTGGGAAAGCCCTCTGCTGCATGATGTGTCTCCCTTCGGAAG	636
Db	1647	AAGAGCAGAGGCACCGAGTTGGGAAAGCCCTCTGCTGCATGATGTGTCTCCCTTCGGAAG	1706
OY	637	GCTGCGTGGGCAATGAGAGCTTGGGGCAATGCTGGGGCAAGTCCGAGCTCTGTGAGACTG	696
Db	1707	GCTGCGTGGGCAATGAGAGCTTGGGGCAATGCTGGGGCAAGTCCGAGCTCTGTGAGACTG	1766
OY	697	CCCCGCCGAGCTGCACCTGCCAGCCTGGCTTCTGAGACCCCTTGAGGTTTTTTGTTTGT	756
Db	1767	CCCCGCCGAGCTGCACCTGCCAGCCTGGCTTCTGAGACCCCTTGAGGTTTTTTGTTTGT	1826

Oy	757	TTTTGTTGTGGTGGTGGTTCCTCCCGCCCTGGGCTCTGCCAGACTGTGGCTTGCCAGAAAAACC	816
Db	1827	TTTTGTTGTGGTGGTGGTTCCTCCCGCCGGGCTCTGCCAGACTGTGGCTTGCCAGAAAAACC	1886
Oy	817	CAGCATCTCTTCTCTGCAGAGGGGCTTCTGAGAGAGAGGATGCTGCTGAGTCAACCCAT	876
Db	1887	CAGCATCTCTTCTCTGCAGAGGGGCTTCTGAGAGAGAGGATGCTGCTGAGTCAACCCAT	1944
Oy	877	GAAAGCAGGACAGTGTCTTCAAGCTGAGGCTGAGACTGCGGGATGTCCTGGGGCTCTGTG	936
Db	1947	GAAAGCAGGACAGTGTCTTCAAGCTGAGGCTGAGACTGCGGGATGTCCTGGGGCTCTGTG	2008
Oy	937	TAGGAGAGAGGTGGCAGCGCTGTGGGAACGGGGTCCCTTAAGTTTGGTCAAGAGGCTTG	996
Db	2007	TAGGAGAGAGGTGGCAGCGCTGTGGGAACGGGGTCCCTTAAGTTTGGTCAAGAGGCTTG	2066
Oy	997	GAAGCATCACCTTAGCGCCAGGTGCAGTGGCTCAGCCCTATGATCCAGACTTTGGGAG	1056
Db	2067	GAAGCATCACCTTAGCGCCAGGTGCAGTGGCTCAGCCCTATGATCCAGACTTTGGGAG	2128
Oy	1057	GCTGAGGGGGGTGGATCACCCTAGAGGTAGAGTTGCAGAACAGCCTTGCGGCAACATGGTA	1116
Db	2127	GCTGAGGGGGGTGGATCACCCTAGAGGTAGAGTTGCAGAACAGCCTTGCGGCAACATGGTA	2186
Oy	1117	AACCCCATCTCTACTAAAATAATACAGAATTAGCCGGGCTGGTGGCGGGCACCTATTATGC	1176
Db	2187	AACCCCATCTCTACTAAAATAATACAGAATTAGCCGGGCTGGTGGCGGGCACCTATTATGC	2246
Oy	1177	CCAGCTACTCGAAGAGCCTGAGGCTGGGAAATCTTTGAACCCGGGAGCGGAGGTTGGAG	1236
Db	2247	CCAGCTACTCGAAGAGCCTGAGGCTGGGAAATCTTTGAACCCGGGAGCGGAGGTTGGAG	2306
Oy	1237	GGAGCCGAGATCAGGCCACTGACATCCAGCCTGGGGAGACAGAGCGGAGTGTCTCAA	1296
Db	2307	GGAGCCGAGATCAGGCCACTGACATCCAGCCTGGGGAGACAGAGCGGAGTGTCTCAA	2366
Oy	1297	AGAAAAAAAAAAAAAGCAGCCGCTCCAAATGCTAACTTGTCTTTGTACACTGATGTGAA	1356
Db	2367	AGAAAAAAAAAAAAAGCAGCCGCTCCAAATGCTAACTTGTCTTTGTACACTGATGTGAA	2426
Oy	1357	AGTCGATGGCCAGAGGGGCCAGGAGGCCACCATTTGAGTGGCTGGCCCTGGGGACA	1416
Db	2427	AGTCGATGGCCAGAGGGGCCAGGAGGCCACCATTTGAGTGGCTGGCCCTGGGGACA	2486
Oy	1417	TACGCACTTCTAACTAGAAATCTGCCAATTTTTAAAAAATAAGTACCACTCAGGCCA	1476
Db	2487	TACGCACTTCTAACTAGAAATCTGCCAATTTTTAAAAAATAAGTACCACTCAGGCCA	2546
Oy	1477	ACAAGCCAAGACAAACCCAAACTCTGCGCACATCCACATCCCACACTGCACTTTGC	1536
Db	2547	ACAAGCCAAGACAAACCCAAACTCTGCGCACATCCACATCCCACACTGCACTTTGC	2606
Oy	1537	ACCCCTGGCCTTCACTCCGGTGTGCCGTGAGGCCCGCGGCTCTTCTCATGTGCTGACTAG	1596
Db	2607	ACCCCTGGCCTTCACTCCGGTGTGCCGTGAGGCCCGCGGCTCTTCTCATGTGCTGACTAG	2666
Oy	1597	CCAAACCATCTCTTTTTCAGGGAATTTTCAGGAACATGAGATGACTGATCTCTGATGCCAT	1656
Db	2667	CCAAACCATCTCTTTTTCAGGGAATTTTCAGGAACATGAGATGACTGATCTCTGATGCCAT	2726
Oy	1657	CTCTCTACTCTCACTACGAGCCTAGACCCCTGCTGCTCCCCAGAGGGGTGGTCTCTTC	1716
Db	2727	CTCTCTACTCTCTCACTACGAGCCTAGACCCCTGCTGCTCCCCAGAGGGGTGGTCTCTTC	2786
Oy	1717	CCCACTCCCCACCTCAATTCCTGGGCCCAAAGGGGTGCCCTGCCACTTTGGTATAGT	1776
Db	2787	CCCACTCCCCACCTCAATTCCTGGGCCCAAAGGGGTGCCCTGCCACTTTGGTATAGT	2846
Oy	1777	GCCAGTGTGATCCCAAGTGGCAGATCTTGTGTCCTGGGCTGTGTGTGCGTGTGCTGGGTGTG	1836
Db	2847	GCCAGTGTGATCCCAAGTGGCAGATCTTGTGTCCTGGGCTGTGTGTGCGTGTGCTGGGTGTG	2906
Oy	1837	TGTAGCCAAAGTGGTAAAGTGAATGGCCCTGCCCTTGAAGCCACTGAAGCTGGATTCCTG	1896

Db	1707	CTGTGGCTGGGCGATGAGACGTTCTGGGGGCAATGCTGGGGCAAGTCCCTTACTCTCTGTGACCTG	1766
Qy	697	CCCCCGCCACCTGACCTGACCTGGCACGCTGGCTTCTGAGCCCTTGGGCTTTTGTGTTGTTTG	756
Nb	1767	CCCCGGCCAGCTGACCTGACCTGACCTGGCTGCTGGAGCCCTTGGGTTTGTGTTGTTTG	1826
Qy	757	TTTGTGTTGTTTGTGTTTGTGTTTCTCCCTGGGGCTGTGCCCCAGCTGTGCTTCCAGAAAACC	816
Db	1827	TTTTTGTGTTGTTTGTGTTTCTCCCTGGGGCTGTGCCCCAGCTGTGCTTCCAGAAAACC	1886
Qy	817	CAGATGCTTTTCTGCGAGAGGGGCTTCTGGAGAGAGAGGATGCTGCGTCAAGTACCCAT	876
Db	1887	CAGATGCTTTTCTGCGAGAGGGGCTTCTGAGAGAGAGGATGCTGCGTCAAGTACCCAT	1946
Qy	877	GAAGACAGGAGAGTGTCTTACGCTTGAGGCTTGAGACAGCGGATGTGCTTGGGGCTGTGTG	936
Db	1947	GAACACAGGAGAGTGTCTTACGCTTGAGGCTTGAGACAGCGGATGTGCTTGGGGCTGTGTG	2006
Qy	937	TAGGAGAGAGTGTGCGACGCTTGAGGGAACGGGGTCTTCAAGTTAGCTCAGAGAGCTTG	996
Nb	2007	TAGGAGAGAGTGTGCGACGCTTGAGGGAACGGGGTCTTCAAGTTAGCTCAGAGAGCTTG	2066
Qy	997	GAAGCATGACCTCAGGCGCAGGTGAGTGTGCTCACGCCATGATCCGACGACCTTGGGAG	1056
Db	2067	GAAGCATGACCTCAGGCGCAGGTGAGTGTGCTCACGCCATGATCCGACGACCTTGGGAG	2126
Qy	1057	GCTAGAGCGGCTGGATCACCCTGAGAGTTAGGAGTTGAGACACAGGCTGGCCAAATGTAT	1116
Db	2127	GCTAGAGCGGCTGGATCACCCTGAGAGTTAGGAGTTGAGACACAGGCTGGCCAAATGTAT	2186
Qy	1117	AACCCATCTCTACTAAAAATACAGAAATTTAGCCGGGC	1154
Db	2187	AACCCATCTCTACTAAAAATACAGAAATTTAGCCGGGC	2224
RESULT 4			
US-08-476-862-1			
: Sequence 1, Application US/08476862			
: Patent No. 6262239			
: GENERAL INFORMATION:			
: APPLICANT: WALLACH, David			
: APPLICANT: BIGDA, Jaack			
: APPLICANT: BELETSKY, Igor			
: APPLICANT: METT, Igor			
: APPLICANT: ENGELMANN, Hartmut			
: TITLE OF INVENTION: TNF INHIBITORS			
: NUMBER OF SEQUENCES: 8			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: BROWDY AND NEIMARK			
: STREET: 419 Seventh Street, N.W.			
: CITY: Washington			
: STATE: D.C.			
: COUNTRY: USA			
: ZIP: 20004			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patentin Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/476,862			
: FILING DATE: 07-JUN-1995			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: IL 107267			
: FILING DATE: 12-OCT-1993			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: IL 94039			
: FILING DATE: 06-APR-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: IL 91229			
: FILING DATE: 06-AUG-1989			

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APPLICATION NUMBER: IL 90339							
FILING DATE: 18-MAY-1989							
ATTORNEY/AGENT INFORMATION:							
NAME: BROMDY, Roger L.							
REGISTRATION NUMBER: 25, 618							
REFERENCE/DOCKET NUMBER: 25, 618							
TELECOMMUNICATION INFORMATION:							
TELEPHONE: 202-628-5197							
TELEFAX: 202-737-3528							
INFORMATION FOR SEQ ID NO: 1:							
SEQUENCE CHARACTERISTICS:							
LENGTH: 2224 base pairs							
TYPE: nucleic acid							
STRANDEDNESS: single							
TOPOLOGY: linear							
MOLECULE TYPE: cdna							
FEATURE:							
NAME/KEY: CDS							
LOCATION: 90..1472							
US-08-476-862-1							
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157	AATGTACCTGCATGCTGTGACAGCTCTGTAGCAGCTTGACACAGCTCAGAGTCTCTCC	216					
1227	AATGTACCTGCATGCTGTGACAGCTCTGTAGCAGCTTGACACAGCTCAGAGTCTCTCC	1286					
217	CAAGCAGGCTCACATGGGAGACACAGATTCACGCCCTCGGAGTCCCGGAAAGACGAG	276					
1287	CAAGCAGGCTCACATGGGAGACACAGATTCACGCCCTCGGAGTCCCGGAAAGACGAG	1346					
277	CAGGTCCCTTCTCCAAAGAGGAATGTGCTTCGGTCACTGAGTGAAGCCAGAGACC	336					
1347	CAGGTCCCTTCTCCAAAGAGGAATGTGCTTCGGTCACTGAGTGAAGCCAGAGACC	1406					
337	CTGCTGGGAGACCGAAGAAAGCCCTTGGAGTGCCTGATGCTGGATGAAG	396					
1407	CTGCTGGGAGACCGAAGAAAGCCCTTGGAGTGCCTGATGCTGGATGAAG	1466					
397	CCCACTTAACCAAGCGCGCTGTGGCTGTGTCTGTAGCAAGGTGGCTGAGCCCTGGACAG	456					
1467	CCCACTTAACCAAGCGCGCTGTGGCTGTGTCTGTAGCAAGGTGGCTGAGCCCTGGACAG	1526					
457	ATGACCTTCGCAAGGAGGCGCTGCTCCCTTCAGAGCCGCCACCACTAGAGACTGTAGAGCTCT	516					
1527	ATGACCTTCGCAAGGAGGCGCTGCTCCCTTCAGAGCCGCCACCACTAGAGACTGTAGAGCTCT	1586					
517	TTCTGGGCGCAAGTTCTCTAGTGCCTTCACAGCGCAGACCTTCCCTGACCTGCAGGCC	576					
1587	TTCTGGGCGCAAGTTCTCTAGTGCCTTCACAGCGCAGACCTTCCCTGACCTGCAGGCC	1646					
577	AAGAGCAGAGGAGGAGGAGTGGGAAAGCTCTGCTGCATAGTGTGTCTCTCGGAAG	636					
1647	AAGAGCAGAGGAGGAGGAGTGGGAAAGCTCTGCTGCATAGTGTGTCTCTCGGAAG	1706					
637	GCTGGGTGGGACATGGACGTTGGGGGATGCTGGGGCAATCTCTGACCTCTGTGACGAG	696					
1707	GCTGGGTGGGACATGGACGTTGGGGGATGCTGGGGCAATCTCTGACCTCTGTGACGAG	1766					
697	CCCCGCCAGCTGACACTGCGCAGCCTGCGCTTGAGAGCCCTTGGGATTTTGTGTTTG	756					
1767	CCCCGCCAGCTGACACTGCGCAGCCTGCGCTTGAGAGCCCTTGGGATTTTGTGTTTG	1826					
757	TTTGTGTTGTTGTTGTTTCTCCCTCGGGCTGTGCCACAGCTGTGGCTTCCAGAAACCC	816					
1827	TTTGTGTTGTTGTTGTTTCTCCCTCGGGCTGTGCCACAGCTGTGGCTTCCAGAAACCC	1886					

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: WI-26 VAA
IMMEDIATE SOURCE:
LIBRARY: WI-26 VAA
CLONE: 1
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1473
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 154..1470
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 88..153
PUBLICATION INFORMATION:
AUTHORS: Smith, Craig A.
AUTHORS: Davis, Terri
AUTHORS: Anderson, Dirk
AUTHORS: Solam, Lisabeth
AUTHORS: Beckmann, M. P.
AUTHORS: Jerzy, Rita
AUTHORS: Dower, Steven K.
AUTHORS: Cosman, David
AUTHORS: Goodman, Raymond G.
TITLE: A Receptor for Tumor Necrosis Factor Defines
TITLE: an Unusual Family of Cellular and Viral Proteins
JOURNAL: Science
VOLUME: 248
PAGES: 1019-1023
DATE: 25-MAY-1990
US-08-650-000-1

Query Match 17.3%, Score 453; DB 2; Length 1641;

Best Local Similarity 96.9%; Pred. No. 1.7e-111;
Matches 462; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 97 GACCCACCCCATCTGTGCTTAGCAGATTCTCCCTGTGGCCATGGAGCCAGGTC 156
|| ||| ||| |
Db 1165 GAGCCCGGGCCAGCACCAGCGGAGCTCAGATTCTCCCTGTGGCCATGGAGCCAGGTC 1224
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PATENT NO. 5395760
APPLICANT: SMITH, CRAIG A.; GOODMAN, RAYMOND G.; BECKMANN, M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR- α AND
B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO: 1
LENGTH: 1641
5395760-1
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66 QY   1059 TGAGCGGGGTGATACACCTGAGAGTTAGAGAGTTTCGAGACCAGCCTGGCCCAACTGTGTA 1118
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72 Db   64929 CCCGCTCTCTAATAAATATACAAAATTTAGCCGGGCGATGTGTGCGAGAGACCTGTATATCCC 64870

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According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:

Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnpb**.

Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 20:03:23 : Search time 127.014 Seconds

(without alignments)
8021.899 Million cell updates/sec

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Perfect score: 2613
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

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2	1034	39.6	2224	10	US-09-800-909-1	Sequence 1, App11
3	1034	39.6	2224	10	US-09-800-908-2	Sequence 2, App11
4	453	17.3	1641	10	US-09-758-124-1	Sequence 1, App11
5	336	12.9	336	10	US-09-777-564-984	Sequence 984, App
6	240.8	9.2	22609	10	US-09-764-877-2146	Sequence 2146, App
7	240.8	9.2	32193	10	US-09-764-877-2147	Sequence 2147, App
8	240	9.2	240	12	US-09-920-300A-1170	Sequence 1170, App
9	240	9.2	240	12	US-10-033-528-1170	Sequence 1170, App
10	239.6	9.2	32193	10	US-09-764-877-2623	Sequence 2623, App
11	238.2	9.1	10252	10	US-09-764-887-442	Sequence 442, App
12	238	9.1	145831	10	US-09-969-708-79	Sequence 79, App1
13	238	9.1	145831	10	US-09-954-456-2116	Sequence 2116, App
14	237.8	9.1	31994	9	US-09-764-904-71	Sequence 71, App1
15	237.8	9.1	31994	9	US-09-764-860-599	Sequence 599, App
16	237.2	9.1	32188	10	US-09-764-860-799	Sequence 799, App
17	235.8	9.0	32146	10	US-09-764-860-797	Sequence 797, App
18	235.8	9.0	58837	10	US-09-982-091A-5	Sequence 5, App11
19	235.4	9.0	32248	10	US-09-764-860-802	Sequence 802, App

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21	235.2	9.0	13117	10	US-09-764-878-224	Sequence 224, App
22	234.8	9.0	197997	10	US-09-822-246-3	Sequence 3, App11
23	234.6	9.0	99014	10	US-09-880-107-3428	Sequence 3428, App
24	234.4	9.0	29629	12	US-10-135-689-3	Sequence 3, App11
25	234.2	9.0	291	10	US-09-964-824A-509	Sequence 509, App
26	234.2	9.0	291	10	US-09-969-347-1	Sequence 1, App11
27	234.2	9.0	15857	10	US-09-764-864-1104	Sequence 1104, App
28	234.2	9.0	24699	10	US-09-764-877-2419	Sequence 2419, App
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32	234	9.0	11337	10	US-09-764-877-2651	Sequence 2651, App
33	234	9.0	174493	10	US-09-804-471A-3	Sequence 3, App11
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35	233.8	8.9	81001	10	US-09-751-877-1	Sequence 1, App11
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37	233.4	8.9	6074	10	US-09-880-107-2378	Sequence 2378, App
38	233.2	8.9	14012	9	US-09-819-994-3	Sequence 3, App11
39	233.2	8.9	75899	10	US-09-834-883-243	Sequence 243, App
40	233	8.9	4766	9	US-09-764-868-1443	Sequence 1443, App
41	233	8.9	14962	10	US-09-764-878-244	Sequence 244, App
42	232.8	8.9	7703	10	US-09-764-887-415	Sequence 415, App
43	232.8	8.9	7703	10	US-09-764-887-456	Sequence 456, App
44	232.4	8.9	400	10	US-09-867-701-8347	Sequence 8347, App
45	232.4	8.9	12493	10	US-09-764-864-1715	Sequence 1715, App

ALIGNMENTS

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Sequence 1187, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE OF INVENTION: Secs
TITLE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
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PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1187
LENGTH: 3683
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ORGANISM: Homo sapiens
US-09-954-456-1187
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Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY	1657	CTCTCTACTCTTACTCAGCTAGGCTAGACCCCTCTCTCTCCCGAGGGGTGGTTCCTCTTC	1716
Db	2727	CTCTCTACTCTTACTCAGCTAGGCTAGACCCCTCTCTCTCCCGAGGGGTGGTTCCTCTTC	2786
QY	1717	CCCACCTCCCACTTCAATTTCTGTGGCCCCAAAGGGCTGCCCTGCACATTGTGTATATC	1776
Db	2787	CCCACCTCCCACTTCAATTTCTGTGGCCCCAAAGGGGTGCCCTGCACATTGTGTATATC	2846
QY	1777	GCGAGTGTGATCCCAAGTGGCAGCTTGTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTG	1836
Db	2847	GCGAGTGTGATCCCAAGTGGCAGCTTGTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTG	2906
QY	1837	TGTAGCCAAAGTCGTAAGTTGAATGGCCCTGTAAACCCACTGAAGCTGGGATTCCTC	1896
Db	2907	TGTAGCCAAAGTCGTAAGTTGAATGGCCCTGTAAACCCACTGAAGCTGGGATTCCTC	2966
QY	1897	CCCAATTAGATCAGCTTCCCCCTCCAGGGCCAGGGCCCTCCAGAGGGGAAACCACTGT	1956
Db	2967	CCCAATTAGATCAGCTTCCCCCTCCAGGGCCAGGGCCCTCCAGAGGGGAAACCACTGT	3026
QY	1957	AGCCTTGGCCGATTTGGGAGAGAACAGTTTAAAGGGCTCTGTGAAAGAGCTCAAGTCTCA	2016
Db	3027	AGCCTTGGCCGATTTGGGAGAGAACAGTTTAAAGGGCTCTGTGAAAGAGCTCAAGTCTCA	3086
QY	2017	GGAGCATGTGGGATTAAGGAAGAAGCATGAATTTGTCTACAGACGAGGGCCAGGGTGATA	2076
Db	3087	GGAGCATGTGGGATTAAGGAAGAAGCATGAATTTGTCTACAGACGAGGGCCAGGGTGATA	3146
QY	2077	AATTGTGATTAATTTCCACTGAGCTTGAAGTTGGAGAGTGAAGCTTGTGGAGGTGGGAGA	2136
Db	3147	AATTGTGATTAATTTCCACTGAGCTTGAAGTTGGAGAGTGAAGCTTGTGGAGGTGGGAGA	3206
QY	2137	GCCCAAGCCATTACCATGTGAGACAAGAAGGGTTTTCCACCCTTGGAAATCAAGATGTACACT	2196
Db	3207	GCCCAAGCCATTACCATGTGAGACAAGAAGGGTTTTCCACCCTTGGAAATCAAGATGTACACT	3266
QY	2197	GGCTGGCTGCAGTACGTGTGACCTGTATCTCAGAGGCTTGAAGGGAGATCATCTGGAGCCC	2256
Db	3267	GGCTGGCTGCAGTACGTGTGACCTGTATCTCAGAGGCTTGAAGGGAGATCATCTGGAGCCC	3326
QY	2257	AGGAGTTTGAAGGCTCAGCAGCAAGCTATGATCTGGCCACTACATCTCAGCTCAGCAACAGA	2316

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Db 3327 AGAGTTTGAGCGCTGCAGGAGTATGATGCGCCACCTACACCTCCAGCCTTGAGCAACANA 3386
Qy 2317 GTAGACCGCTGTCTTTAAAGAAAAAAGTCAGACTCTGGGACTGCCAGGTTTCTG 2376
Db 3387 GTGAGACCGCTGTCTTTAAAGAAAAAAGTCAGACTCTGGGACTGCCAGGTTTCTG 3446
Qy 2377 CCCACATTTGAGCCACATATGAGCATGATGAGCGACCGACCTGCTGTGACAGTCTT 2436
Db 3447 CCCACATTTGAGCCACATATGAGCATGATGAGCGACCGACCTGCTGTGAGCACTCT 3506
Qy 2437 GGGAGAACCTCAGACTTCTCTTGGCATCAGAGGCGAGCGGAAACGATGATTTGGAG 2496
Db 3507 GGGAGAACCTCAGACTTCTCTTGGCATCAGAGGCGAGCGGAAACGATGATTTGGAG 3566
Qy 2497 ACTCTGTGGGCGCTTGGTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 2556
Db 3567 ACTCTGTGGGCGCTTGGTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 3626
Qy 2557 CACTGATGCTGAGCGCATTCCTCTTATCAATAAACCTGTTTGTAAAAAAA 2613
Db 3627 CACTGATGCTGAGCGCATTCCTCTTATCAATAAACCTGTTTGTAAAAAAA 3683

RESULT 2
US-09-800-909-1
: Sequence 1. Application US/09800909
: Patent No. US20010019833A1
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BIGDA, Jacek
: APPLICANT: BELETSKY, Igor
: APPLICANT: MERT, Igor
: APPLICANT: ENGELMANN, Hartmut
: TITLE OF INVENTION: TNF INHIBITORS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/800.909
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/476,862
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 94039
: FILING DATE: 06-APR-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 91229
: FILING DATE: 06-AUG-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 90339
: FILING DATE: 18-MAY-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH-12A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:

: LENGTH: 2224 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 90..1472
US-09-800-909-1
Query Match 39.6%; Score 1034; DB 10; Length 2224;
Best Local Similarity 98.6%; Pred. No. 9,6e-211;
Matches 1043; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 97 GACCCCAACCCATCTTGTGCTTAGACAGATTTCTCCCTGTGTCATAGGACCAAGTC 156
Db 1167 GAGGCCCGGCGAGACCGCGAGAGCTCAGATTTCTCCCTGTGTCATAGGACCAAGTC 1226
Qy 157 AATGTCACCTGATGCTGAAGCTGTAGAGCTGTAGACAGCTGTACACAGCTCAGAGTCTCTCC 216
Db 1227 AATGTCACCTGATGCTGAAGCTGTAGAGCTGTAGAGCTGTACACAGCTCAGAGTCTCTCC 1286
Qy 217 CAAGCCAGCTCCAGCAATGGAGACACAGATTCAGACCCCTTGAGATCCCGAAGACAG 276
Db 1287 CAAGCCAGCTCCAGCAATGGAGACACAGATTCAGACCCCTTGAGATCCCGAAGACAG 1346
Qy 277 CAGTCCCTTCTCCAGAGGAATGTGCTTGTGTCACAGCTGTAGAGCCAGAGACC 336
Db 1347 CAGTCCCTTCTCCAGAGGAATGTGCTTGTGTCACAGCTGTAGAGCCAGAGACC 1406
Qy 337 CTGCTGGGAGACACCGAAGAACGCCCTGCTGAGAGCCTGATGCTGGATAG 396
Db 1407 CTGCTGGGAGACACCGAAGAACGCCCTGCTGAGAGCCTGATGCTGGATAG 1466
Qy 397 CCAGTTAACAGGCGGCTGTGGCTGTGTGTAGCCAAAGTGAGGCTGAGCCCTGAGG 456
Db 1467 CCAGTTAACAGGCGGCTGTGGCTGTGTGTAGCCAAAGTGAGGCTGAGCCCTGAGG 1526
Qy 457 ATGACCTGCGCAAGGGGCGCTGTGCTTTCAGAGCCCGACCACTAGAGCTGTGAGGCTCT 516
Db 1527 ATGACCTGCGCAAGGGGCGCTGTGCTTTCAGAGCCCGACCACTAGAGCTGTGAGGCTCT 1586
Qy 517 TTCTGGGCGCAAGTTCTCTAGTGCCTCCACAGCGGAGGCTCTCTGACCTCAGAGCC 576
Db 1587 TTCTGGGCGCAAGTTCTCTAGTGCCTCCACAGCGGAGGCTCTCTGACCTCAGAGCC 1646
Qy 577 AAGACAGAGGCGAGGCTGTGGGAAAGCCCTCTGCTCATGTGTGTCTCTCGAAG 636
Db 1647 AAGACAGAGGCGAGGCTGTGGGAAAGCCCTCTGCTCATGTGTGTCTCTCGAAG 1706
Qy 637 GCTGGCTGGGATGAGAGCTGTGGGGCATGTGGGGCAAGTCCCTGACTCTGTGACCTG 696
Db 1707 GCTGGCTGGGATGAGAGCTGTGGGGCATGTGGGGCAAGTCCCTGACTCTGTGACCTG 1766
Qy 697 CCGCGCCAGCTGCACCGCTGCAGCGCTGTCTGGAGCCCTTGAGGTTTGTGTTG 756
Db 1767 CCGCGCCAGCTGCACCGCTGCAGCGCTGTCTGGAGCCCTTGAGGTTTGTGTTG 1826
Qy 757 TTTGTTGTTGTTGTTGTTCTCCCTGTGGGCTGTGCCAGCTGTGCTTCAGAAAAACC 816
Db 1827 TTTGTTGTTGTTGTTGTTCTCCCTGTGGGCTGTGCCAGCTGTGCTTCAGAAAAACC 1886
Qy 817 CAGCATCTTTCTGCAAGAGGGGCTTTCTGAGAGAGAGAGATGTGCTGATGACCAT 876
Db 1887 CAGCATCTTTCTGCAAGAGGGGCTTTCTGAGAGAGAGAGATGTGCTGATGACCAT 1946
Qy 877 GAAGACAGAGAGTGTTCACAGCTGAGGCTGAGACTCGGAGATGTCTCTGGGCTGTG 936
Db 1947 GAAGACAGAGAGTGTTCACAGCTGAGGCTGAGACTCGGAGATGTCTCTGGGCTGTG 2006
Qy 937 TAGGAGAGAGTGTTCACAGCTGAGGAGCGGAGTCTTCAAGTTAGCTAGAGGCTTG 996
Db 2007 TAGGAGAGAGTGTTCACAGCTGAGGAGCGGAGTCTTCAAGTTAGCTAGAGGCTTG 2066

QY 997 GAAGCATCACCTGAGGCGAGGTGCTAGTGGCTACGCCCTATGATCCAGCATTGGGAG 1056
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Db 2067 GAAAGCATCACCTGAGGCGAGGTGCTAGTGGCTACGCCCTATGATCCAGCATTGGGAG 2126
QY 1057 GCTGAGGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 1116
|||||
Db 2127 GCTGAGGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 2186
QY 1117 AACCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 1154
|||||
Db 2187 AACCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 2224

RESULT 3

US-09-800-908-2

Sequence 2, Application US/09800908

Patent No. US2002011162A1

GENERAL INFORMATION:

APPLICANT: WALLACH, David

BIGDA, Jacek

BELETSKY, Igor

METT, Igor

TITLE OF INVENTION: TNF LIGANDS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/800.908

FILING DATE: 08-Mar-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,347

FILING DATE: <unknown>

APPLICATION NUMBER: IL 106271

FILING DATE: 08-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, G. Kevin

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: WALLACH-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ. ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2224 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 90..1472

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-800-908-2

Query Match 39.6% Score 1034: DB 10: Length 2224:
Best Local Similarity 98.6% Pred. No. 9, 6e-211:
Matches 1043: Conservative 0: Mismatches 15: Indels 0: Gaps 0:

QY 97 GACCCGACCCCATCTGTGCTTGAAGATTCTCCCTGGCCATGGAGCCAGGTC 156
||| ||| ||| | |||||||||||||||||||||||||||||||||||||||

Db 1167 GAGGCCCGGGCCAGCACCAGGAGCTCAGATTCTCCCTGGTGGCCATTGGACCCAGGTC 1226
QY 157 AATGTCACCTGATGTTGATGACCTGTGTACACCTGTGACACACAGCTCAGTCTCC 216
|||||
Db 1227 AATGTCACCTGATGTTGATGACCTGTGTACACCTGTGACACACAGCTCAGTCTCC 1286
QY 217 CAAGCAGCTCCACATGAGGAGACACAGATTCCACCTCTGAGTCTCCCGAAGAGCAG 276
|||||
Db 1287 CAAGCAGCTCCACATGAGGAGACACAGATTCCACCTCTGAGTCTCCCGAAGAGCAG 1346
QY 277 CAGGTCCTCTTCCCAAGGAGGAATGTGCTTTTGGGTACACAGCTGAGAGCCAGAGACC 336
|||||
Db 1347 CAGGTCCTCTTCCCAAGGAGGAATGTGCTTTTGGGTACACAGCTGAGAGCCAGAGACC 1406
QY 337 CTGCTGGGGAGACACGGAAGAAGACCCCTGGCCCTTTGAGTCTCTGATGCTGGATAG 396
|||||
Db 1407 CTGCTGGGGAGACACGGAAGAAGACCCCTGGCCCTTTGAGTCTCTGATGCTGGATAG 1466
QY 397 CCCAGTTAACACAGCGCGGTGGGCTGTGTCTAGCACAAGGTTGGGCTGAGCCCTGGCAG 456
|||||
Db 1467 CCCAGTTAACACAGCGCGGTGTGGGCTGTGTCTAGCACAAGGTTGGGCTGAGCCCTGGCAG 1526
QY 457 ATGACCTCTCGAAGGGGCCCTGTCTTCAGAGGCCCCACACCACTAGAGCTGAGGCTCT 516
|||||
Db 1527 ATGACCTCTCGAAGGGGCCCTGTCTTCAGAGGCCCCACACCACTAGAGCTGAGGCTCT 1586
QY 517 TTCTGGGCAAGTTCTCTAGTGGCCCTCCACAGCCGAGCCTCTCTGAGCTGAGGCC 576
|||||
Db 1587 TTCTGGGCAAGTTCTCTAGTGGCCCTCCACAGCCGAGCCTCTCTGAGCTGAGGCC 1646
QY 577 AAGAGCAGAGGAGGAGAGTTGGGGAAGCCCTCTGCTGCTGATGTTGCTCTCTGCAAG 636
|||||
Db 1647 AAGAGCAGAGGAGGAGAGTTGGGGAAGCCCTCTGCTGCTGATGTTGCTCTCTGCAAG 1706
QY 637 GCTGCTGGGCAATGACCTGTGGGGCATGTGGGGCAAGTCCCTGACTCTGTGACTG 696
|||||
Db 1707 GCTGCTGGGCAATGACCTGTGGGGCATGTGGGGCAAGTCCCTGACTCTGTGACTG 1766
QY 697 CCCCGCCAGCTGACACCTGCAAGCCGCTTGTGAGGCCCTTGGTGTGTTGTTGTTG 756
|||||
Db 1767 CCCCGCCAGCTGACACCTGCAAGCCGCTTGTGAGGCCCTTGGTGTGTTGTTGTTG 1826
QY 757 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 816
|||||
Db 1827 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1886
QY 817 CAGCATCTCTTCTGACAGAGGGCTTTTGTGAGAGAGAGGATGCTGCTGATCACCAT 876
|||||
Db 1887 CAGCATCTCTTCTGACAGAGGGCTTTTGTGAGAGAGGATGCTGCTGATCACCAT 1946
QY 877 GAAAGCAGAGCAGTCTTCTGAGCTGAGGCTGAGAGTGGGGATGGTCTGGGGCTCTGTG 936
|||||
Db 1947 GAAAGCAGAGCAGTCTTCTGAGCTGAGGCTGAGAGTGGGGATGGTCTGGGGCTCTGTG 2006
QY 937 TAGGAGAGAGTGGAGCCCTGTAGGGAACGGGCTCTTCAAGTTAGCTCAGAGAGCTTG 996
|||||
Db 2007 TAGGAGAGAGTGGAGCCCTGTAGGGAACGGGCTCTTCAAGTTAGCTCAGAGAGCTTG 2066
QY 997 GAAAGCATCACCTGAGGCGAGGTGCTAGTGGCTACGCCCTATGATCCAGCATTGGGAG 1056
|||||
Db 2067 GAAAGCATCACCTGAGGCGAGGTGCTAGTGGCTACGCCCTATGATCCAGCATTGGGAG 2126
QY 1057 GCTGAGGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 1116
|||||
Db 2127 GCTGAGGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 2186
QY 1117 AACCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 1154
|||||
Db 2187 AACCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 2224

RESULT 4
US-09-738-124-1

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: Sequence 1, Application US/09758124
: Patent No. US2002006391A1
: GENERAL INFORMATION:
: APPLICANT: SMITH, Craig A.
: APPLICANT: GOODMAN, Raymond G.
: APPLICANT: BECKMANN, W. Patricia
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
: FILE REFERENCE: A7895
: CURRENT APPLICATION NUMBER: US/09/758,124
: CURRENT FILING DATE: 2001-01-12
: PRIOR APPLICATION NUMBER: 08/953,268
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 08/555,629
: PRIOR FILING DATE: 1995-11-09
: PRIOR APPLICATION NUMBER: 08/468,453
: PRIOR FILING DATE: 1995-06-06
: PRIOR APPLICATION NUMBER: 08/038,765
: PRIOR FILING DATE: 1993-03-13
: PRIOR APPLICATION NUMBER: 07/523,635
: PRIOR FILING DATE: 1990-05-10
: PRIOR APPLICATION NUMBER: 07/421,417
: PRIOR FILING DATE: 1989-10-13
: PRIOR APPLICATION NUMBER: 07/405,370
: PRIOR FILING DATE: 1989-09-11
: PRIOR APPLICATION NUMBER: 07/403,241
: PRIOR FILING DATE: 1989-09-05
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1641
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (88)..(1473)
: NAME/KEY: mat_peptide
: LOCATION: (154)..(1470)
: NAME/KEY: sig_peptide
: LOCATION: (88)..(153)
: US-09-758-124-1

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Query Match 17.3%; Score 453; DB 10; Length 1641;

Best Local Similarity 96.9%; Pred. No. 2e-87;

Matches 462; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Oy 97 GACCCACCCATCTTGTCTAGACAGATTCTTCCCTGGTGGCCATGSGAGCCAGAGTC 156
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1165 GAGGCCGGGGCCACACACGGGAGAGTCAGATTCTTCCCTGTGGCCATGSGAGCCAGAGTC 1224

Oy 157 AATGTACCTGACATGTGAACGCTGTGTAGACGCTTGACACAGCTCAGAGTCTCTCTCC 216
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1225 AATGTACCTGACATGTGAACGCTGTGTAGACGCTTGACACAGCTCAGAGTCTCTCTCC 1284

Oy 217 CAACCCAGCTCCCAATGGGAGACACAGATTTCAGCCCTCGGAGTCCCGGAGGAGAGAG 276
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1285 CAACCCAGCTCCCAATGGGAGACACAGATTTCAGCCCTCGGAGTCCCGGAGGAGAGAG 1344

Oy 277 CAGTCCCTTCTTCCAGAGGAATGTGCTTTCGTCACAGCTGAGAGCCAGAGACC 336
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1345 CAGTCCCTTCTTCCAGAGGAATGTGCTTTCGTCACAGCTGAGAGCCAGAGACC 1404

Oy 337 CTGCTGGGAGACACCGAAGAAAGCCCTCCCTTGGAGTGCCTGATGCTGGGATGAAG 396
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1405 CTGCTGGGAGACACCGAAGAAAGCCCTCCCTTGGAGTGCCTGATGCTGGGATGAAG 1464

Oy 397 CCCAGTTAACGAGCGGCTGTGGGCTGTGTGTAGCCCAAGTGGGCTGAGACCTTGCCAGG 456
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1465 CCCAGTTAACGAGCGGCTGTGGGCTGTGTGTAGCCCAAGTGGGCTGAGACCTTGCCAGG 1524

Oy 457 ATGACCTTGCAGAGGGGCTGTGCTCTTCCAGGCCCCCAGCACTAGAGACTGTAGGCTCT 516
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1525 ATGACCTTGCAGAGGGGCTGTGCTCTTCCAGGCCCCCAGCACTAGAGACTGTAGGCTCT 1584

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Oy 517 TTCTGGGCCAAGTCTCTAGTGGCCCTCCACAGCCGACCCCTCTGACCTGCAG 573
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1585 TTCTGGGCCAAGTCTCTAGTGGCCCTCCACAGCCGACCCCTCTGACCTGCAG 1641

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RESULT 5

US-09-777-564-984/C

: Sequence 984, Application US/09777564

: Patent No. US20020022591A1

: GENERAL INFORMATION:

: APPLICANT: Algate, Paul A.

: APPLICANT: Mannion, Jane

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

: FILE REFERENCE: 210121.493

: CURRENT APPLICATION NUMBER: US/09/777,564

: CURRENT FILING DATE: 2001-02-05

: SOFTWARE: FastSeq for Window Version 4.0

: SEQ ID NO 984

: LENGTH: 336

: TYPE: DNA

: ORGANISM: Homo sapiens

: US-09-777-564-984

Query Match 12.9%; Score 336; DB 10; Length 336;

Best Local Similarity 100.0%; Pred. No. 9.5e-63;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1778 CCAGTGTGATCCCAAGTGCACGCTTGTGTGCTGTGCTGTGTGCTGTGCTGTGTGT 1837
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 336 CCAGTGTGATCCCAAGTGCACGCTTGTGTGCTGTGCTGTGTGCTGTGCTGTGTGT 277

Oy 1838 GTAGCCAAAGTGGGTTAAGTTGAATGGCTGCTTAAGCCACTGAAGCTGGATTCCTCC 1897
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 276 GTAGCCAAAGTGGGTTAAGTTGAATGGCTGCTTAAGCCACTGAAGCTGGATTCCTCC 217

Oy 1898 CCATTAGACTCAGCTTCCCTCCCGAGGAGCCAGGAGCCCTGAGAGGGGAAACAGTGTGA 1957
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 216 CCATTAGACTCAGCTTCCCTCCCGAGGAGCCAGGAGCCCTGAGAGGGGAAACAGTGTGA 157

Oy 1958 GCCTTGCCTCCGATTTCTGGGAGAGCAGGTTGAGGGGCTCTGTAAGAGCTCAGTCTCAG 2017
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 156 GCCTTGCCTCCGATTTCTGGGAGAGCAGGTTGAGGGGCTCTGTAAGAGCTCAGTCTCAG 97

Oy 2018 GAGCATGGGGATAAAGAGAAAGCAATGAATGTCTAGCAGAGCAGGGGAGGATGAATA 2077
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 96 GAGCATGGGGATAAAGAGAAAGCAATGAATGTCTAGCAGAGCAGGGGAGGATGAATA 37

Oy 2078 ATTGTGATTAATTCACATGACACTTGAGCTTGAGCAG 2113
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 36 ATTGTGATTAATTCACATGACACTTGAGCTTGAGCAG 1

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RESULT 6

US-09-764-877-2146/C

: Sequence 2146, Application US/09764877

: Patent No. US20020147140A1

: GENERAL INFORMATION:

: APPLICANT: Rosen et al.

: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

: FILE REFERENCE: PC005

: CURRENT APPLICATION NUMBER: US/09/764,877

: CURRENT FILING DATE: 2001-01-17

: Prior application data removed - refer to PAM or file wrapper

: NUMBER OF SEQ ID NOS: 4031

: SOFTWARE: Patentin Ver. 2.0

: SEQ ID NO 2146

: LENGTH: 22609

: TYPE: DNA

: ORGANISM: Homo sapiens

: US-09-764-877-2146

TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-528-1170

Query Match
Best Local Similarity 100.0%; Score 240; DB 12; Length 240;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2366 CCAGGTTTCTGCCCATTTGGACATTCAGGAGCATGATGAGCGGACCTGCCCCCTGG 2425
DB 1 CCAGGTTTCTGCCCATTTGGACATTCAGGAGCATGATGAGCGGACCTGCCCCCTGG 60
QY 2426 TCGACAGTCTTGAGAACTTCAGGCTTCCTTGGCATCAGAGGAGCGCGGAGCGGA 2485
DB 61 TCGACAGTCTTGAGAACTTCAGGCTTCCTTGGCATCAGAGGAGCGCGGAGCGGA 120
QY 2486 TGAATTTGAGACACTCTGTTGGGCGCTTGGTTCCTTGTGTGTGTGTGTGTGTGTGT 2545
DB 121 TGAATTTGAGACACTCTGTTGGGCGCTTGGTTCCTTGTGTGTGTGTGTGTGTGTGT 180
QY 2546 ATGAAGTTTGGACCTGTATGCTGAGCGGACATTCCTGCTTATCAATAACCTGTTGTTT 2605
DB 181 ATGAAGTTTGGACCTGTATGCTGAGCGGACATTCCTGCTTATCAATAACCTGTTGTTT 240

RESULT 10
US-09-764-877-2623/C
Sequence 2623, Application US/09764877
Patent No. US2002014710A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2623
LENGTH: 32193
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2623

Query Match
Best Local Similarity 9.2%; Score 239; DB 10; Length 32193;
Matches 263; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1009 TCAGGCGAGTGCAGTGCCTCAGCGCTATGATCCAGCACTTTGGAGGCTGAGCGGCT 1068
DB 13658 TCAGGCGAGTGCAGTGCCTCAGCGCTATGATCCAGCACTTTGGAGGCTGAGCGGCT 13599
QY 1069 GCATACCTGAGGTTAGAGTTCCAGACCCAGCTGCGCAACATGTTAAACCCACTCTCT 1128
DB 13598 GCATACCTGAGGTTAGAGTTCCAGACCCAGCTGCGCAACATGTTAAACCCACTCTCT 13539
QY 1129 ACTAAATATACAGAAATATAGCGGCGTGTGGGCGCACTTATAGTCCGACTACTCAG 1188
DB 13538 ACTAAATATACAGAAATATAGCGGCGTGTGGGCGCACTTATAGTCCGACTACTCAG 13479
QY 1189 AAGCCTGAGGCTGGGAAATGCTTTGAACCCGGAAGCGAGGTTGAGAGGAGCCGAGATC 1248
DB 13478 AAGCCTGAGGCTGGGAAATGCTTTGAACCCGGAAGCGAGGTTGAGAGGAGCCGAGATC 13419
QY 1249 ACGCAGTGCAGTCCAGGCTGGGCGAGACAGAGAGAGTCTCTCCAAAAGAAAAA 1308
DB 13418 ACGCAGTGCAGTCCAGGCTGGGCGAGACAGAGAGAGTCTCTCCAAAAGAAAAA 13359
QY 1309 AA 1310
DB 13358 AA 13357

RESULT 11
US-09-764-887-442
Sequence 442, Application US/09764887
Patent No. US20020042096A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA113
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 442
LENGTH: 10252
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-887-442

Query Match
Best Local Similarity 9.1%; Score 238.2; DB 10; Length 10252;
Matches 261; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1012 GCCCAGTGCAGTGCCTCAGCGCTATGATCCAGCACTTTGGAGGCTGAGCGGCTGA 1071
DB 8391 GCCCAGTGCAGTGCCTCAGCGCTATGATCCAGCACTTTGGAGGCTGAGCGGCTGA 8450
QY 1072 TCACCTGAGGTTAGAGTTGAGACAGCAGCTGCGCAACATGTAAACCCATCTTACT 1131
DB 8451 TCACCTGAGGTTAGAGTTGAGACAGCAGCTGCGCAACATGTAAACCCATCTTACT 8510
QY 1132 AAAAATACAAATTTAGCCGCGCTGTTGGCGGACACTTATGCCAGTACTCAGAG 1191
DB 8511 AAAAATACAAATTTAGCCGCGCTGTTGGCGGACACTTATGCCAGTACTCAGAG 8570
QY 1192 CTTGAGGCTGGAAATCTGTTGAACCCGGAAGCGAGGTTGAGAGGAGCGGAGATCAG 1251
DB 8571 CTTGAGGCTGGAAATCTGTTGAACCCGGAAGCGAGGTTGAGAGGAGCGGAGATCAG 8630
QY 1252 CCACCTGACTCCAGCTGCGGCGAGACAGAGAGTGTCTCAAAAAGAAAAA 1310
DB 8631 CCACCTGACTCCAGCTGCGGCGAGACAGAGAGTGTCTCAAAAAGAAAAA 8689

RESULT 12
US-09-969-708-79
Sequence 79, Application US/09969708
Patent No. US20020102532A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
FILE OF INVENTION: Sets
CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
SEQ ID NO 79
LENGTH: 145831
TYPE: DNA
ORGANISM: Homo sapiens
US-09-969-708-79

Query Match
Best Local Similarity 9.1%; Score 238; DB 10; Length 145831;
Matches 262; Conservative 0; Mismatches 40; Indels 0; Gaps 0;


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1  APPLICANT: Rosen et al.
2
3  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
4
5  FILE REFERENCE: PC008
6
7  CURRENT APPLICATION NUMBER: US/09/764,860
8
9  CURRENT FILING DATE: 2001-01-17
10
11 Prior application data removed - consult PALM or file wrapper
12
13 NUMBER OF SEQ ID NOS: 1198
14
15 SOFTWARE: PatentIn Ver. 2.0
16
17 SEQ ID NO: 599
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19 LENGTH: 31994
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21 TYPE: DNA
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23 ORGANISM: Homo sapiens
24
25 US-09-764,860-599

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Query Match	9.1%;	Score 237.8;	DB 10;	Length 31994;
Best Local Similarity	85.0%;	Pred. No. 2.1e-41;		
Matches 266;	Conservative 0;	Mismatches 47;	Indels 0;	Gaps 0;

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OY	1298	GAATAAAAAAAAAA	1310
Db	18079	AAAAAAAAAAAAAA	18067

Search completed: December 5, 2002, 23:53:17
Job time : 1341.01 secs

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Welnstock, G. and Gibbs, R.

Unpublished
Direct Submission
2 (bases 1 to 103287)
Worley, K.C.
Submitted (11-OCT-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 103287)
Worley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117994.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HCGG
Center clone name: RP11-502H22
----- Summary Statistics
Sequencing vector: M13;
Chemistry: Dye-Primer Bodypy: 37% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 117633 bases at least Q40
Consensus quality: 136061 bases at least Q30
Estimated insert size: 141518; sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

FEATURES

source

1..103287
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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11410: gap of unknown length
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13930: contig of 2520 bp in length
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16331: gap of unknown length
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70208
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Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GTGATCTGCAGATGACATCAC 22
      1111 11111111 11111111
Db 76175 GTGACTGCAGAGACATCAC 76196

RESULT 2
CNS01DRV/c      194871 bp      DNA      linear      PRI 04-SEP-2001
LOCUS
DEFINITION      Human chromosome 14 DNA sequence BAC R-1017G21 of library RPCI-11
ACCESSION      AL118558
VERSION      AL118558.6 GI:15485141
KEYWORDS      HTG; HTGS_ACTIVEFIN.
SOURCE      human
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS      Heilig, R., Petit, J. L., Vico, V., Dasilva, C., Robert, C., Winkler, P.,
      Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
      Leroy, M., Eckenberg, R., Bruls, T., debernardinis, V., Cruaud, C.,
      Gyspy, G., Saurin, W. and Weissenbach, J.
      Sequencing of the human chromosome 14
      Unpublished
      2 (bases 1 to 194871)
      Genoscope.
      Direct Submission
      Submitted (04-SEP-2001) Genoscope - Centre National de Sequencage :
      BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
      - Web : www.genoscope.cns.fr)
      On Sep 6, 2001 this sequence version replaced gi:14571656.
      ----- Genome Center
      Center: Genoscope / Centre National de Sequencage
      Center code: GS
      Web site: http://www.genoscope.cns.fr/
      Contact: seqref@genoscope.cns.fr
      -----
      The following BAC sequence is oriented from the T7 to the SP6 end.
      Upstream BAC (overlapping the T7 end) : C-2017C7
      Downstream BAC (overlapping the SP6 end) : R-114H15 (AC-AL133223)
      ----- Summary Statistics
      Assembly program: Phrap; version 2.0
      Quality coverage: 9.00x in Q20 bases; sum-of-coverage
      -----
      Overall quality chart :
      Range      : bases
      0      :
      1 - 9      : 1
      10 - 19     : 1
      20 - 29     : 36
      30 - 39     : 176
      40 - 49     : 2561
      50 - 59     : 6668
      60 - 69     : 12185
      70 - 79     : 30197
      80 - 89     : 70225
      90 - 99     : 72822
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      Percentage of bases with a quality value >= 40 : 99 %.
      Location/Qualifiers
      1. 194871
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="14"

BASE COUNT      49542 a 46484 c 46814 g 52031 t
ORIGIN
Query Match      85.5%; Score 18.8; DB 9; Length 194871;
Best Local Similarity 90.9%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GTGATCTGCAGATGACATCAC 22
      1111 11111111 11111111
Db 138389 GTGACTGCAGAGACATCAC 138368

RESULT 3

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AC108413 61823 bp DNA linear HTG 27-JAN-2002
LOCUS Mus musculus clone RP23-472M11, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC108413
ACCESSION AC108413.1 GI:18377223
VERSION HTG: HTGS_PHASE0.
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 61823)
Birten,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus clone RP23-472M11
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 61823)
Birten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barne,N., Bastien,V., Boguslavsky,L., Boukigalter,B.,
Brown,A., Camarata,J., Camporiano,A., Chang,J., Chazaro,B.,
Choepl,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
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Rovelli,M., Roy,A., Santos,R., Schauer,S., Schnupack,R., Seaman,S.,
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Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliou,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20284
Center clone name: 472_M_11

* NOTE: This record contains 77 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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* 4010 4707: contig of 698 bp in length
* 4708 4807: gap of 100 bp
* 4808 5430: contig of 683 bp in length
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* 49827 49926: gap of 100 bp
* 49927 50641: contig of 715 bp in length
* 50642 50741: gap of 100 bp
* 50742 51413: contig of 672 bp in length
* 51414 51513: gap of 100 bp
* 51514 52212: contig of 699 bp in length
* 52213 52312: gap of 100 bp
* 52313 53043: contig of 731 bp in length
* 53044 53143: gap of 100 bp
* 53144 53858: contig of 715 bp in length
* 53859 53958: gap of 100 bp
* 53959 54662: contig of 704 bp in length
* 54663 54762: gap of 100 bp
* 54763 55475: contig of 713 bp in length
* 55476 55575: gap of 100 bp

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Query Match 83.6% Score 18.4; DB 2; Length 61823;
 Best Local Similarity 95.0% Pred. No. 3.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGATCTGCAAGTGAAGTCA 21
 DB 45566 TGATCTGCAAGTGAAGTCA 45585

RESULT 4 AC108049 89604 bp DNA linear PRI 23-MAR-2002
 LOCUS AC108049 Homo sapiens BAC clone RP11-325P16 from 2, complete sequence.
 ACCESSION AC108049.5 GI:19310337
 VERSION AC108049.5
 KEYWORDS HTG.
 SOURCE Homo sapiens.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 89604)
 AUTHORS Sulston, J. E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8, -1, 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 89604)
 AUTHORS Harris, A. and Cotton, M.
 TITLE The sequence of Homo sapiens BAC clone RP11-325P16
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 89604)
 AUTHORS Waterston, R. H.
 TITLE Direct Submission
 JOURNAL Submitted (24-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 89604)
 AUTHORS Waterston, R. H.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 89604)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Mar 9, 2002 this sequence version replaced gi:18653771.

 Center: Washington University Genome Sequencing Center
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@wustl.wustl.edu

 Summary Statistics

 Center project name: H_NH0325P16

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Tatenno, M., Catanesi, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-103L19, 2000 bp overlap; the clone sequenced to the right is RP11-19J8. Actual end of this clone is at base position 89604 of RP11-325P16.

Polymorphisms have been identified between AC016994, AC096663, and AC108049.

FEATURES Data from AC016994 was used to finish this clone, AC108049.

Source 1. 89604
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-325P16"
 /clone_lib="RPC1-11"
 238..631
 repeat_region /rpt_family="MaLR"
 953..1276
 /rpt_family="MER1_type"
 1299..1464
 /rpt_family="Alu"
 1474..1760
 /rpt_family="Alu"
 1924..2153
 /rpt_family="L1"
 2845..2896
 /rpt_family="G-rich"
 3681..3820
 /rpt_family="L2"
 4186..4351
 /rpt_family="MER1_type"
 4473..44926
 /rpt_family="ERV1"
 7234..7342
 /rpt_family="L1"
 7343..7726
 /rpt_family="MaLR"
 7727..9320
 /rpt_family="L1"
 9522..9547
 /rpt_family="AT-rich"
 10172..10467
 /rpt_family="Alu"
 10602..11068
 /rpt_family="MER2_type"
 11114..11230
 /rpt_family="MER2_type"
 12016..12216
 /rpt_family="MaLR"
 12783..12905
 /rpt_family="(TA)n"
 13296..13317
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 13999..14064
 /rpt_family="L2"
 14065..14077
 /rpt_family="MaLR"
 14078..14383
 /rpt_family="Alu"
 14097..14221
 /note="match to EST A1392740 (NID:94222287) tg23f02.x1"
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 15411..15525
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 16245..17651
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 17891..17961
 /rpt_family="MaLR"
 18236..18316
 /rpt_family="ERV1"
 18443..18817
 /rpt_family="ERV1"

repeat_region 19100..19244
 /rpt_family="L1"
 repeat_region 19290..19489
 /rpt_family="L1"
 repeat_region 20697..20790
 /rpt_family="L1"
 repeat_region 20808..20854
 /rpt_family="(CTTA)n"
 repeat_region 20855..21082
 /rpt_family="L1"
 repeat_region 21099..22284
 /rpt_family="L1"
 repeat_region 22287..22477
 /rpt_family="L1"
 repeat_region 22478..22815
 /rpt_family="MaLR"
 repeat_region 22816..23308
 /rpt_family="L1"
 repeat_region 23418..23495
 /rpt_family="Mariner"
 24157..24180
 /rpt_family="AT-rich"
 24612..24695
 /rpt_family="MIR"
 24738..24799
 /rpt_family="L1"
 repeat_region 24800..25091
 /rpt_family="Alu"
 repeat_region 25092..25501
 /rpt_family="L1"
 repeat_region 25581..25673
 /rpt_family="L1"
 repeat_region 25985..26017
 /rpt_family="(TC)n"
 26507..26954
 /rpt_family="MaLR"
 27792..27815
 /rpt_family="(TC)n"
 28116..28377
 /rpt_family="(TA)n"
 repeat_region 28378..28654
 /rpt_family="Alu"
 repeat_region 29399..29590
 /rpt_family="ERV1"
 repeat_region 29591..29875
 /rpt_family="Alu"
 repeat_region 29877..30106
 /rpt_family="ERV1"

Query Match 83.6% Score 18.4; DB 9; Length 89604;
 Best Local Similarity 95.0%; Pred. No. 3,3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TGATCTGCAAGTGAACCTCA 21
 Db 20611 TGATCTGCAAGCTGAACCTCA 20630

RESULT 5
 AC112572 160505 bp DNA linear HTG 14-JUL-2002
 LOCUS Rattus norvegicus clone CH230-7M8, *** SEQUENCING IN PROGRESS ***
 DEFINITION 73 unordered pieces.
 ACCESSION AC112572
 VERSION AC112572.2 GI:21731408
 KEYWORDS HTG: HTGS, PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 160505)
 AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., All-ouman,F.R., Allen,C.,

Alsbrooks, S.L., Amaralunga, H.C., Are, J.R., Ayele, M., Banks, T., Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Loulsegod, H., Lopez, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Monabadi, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Ogund, M., Okunnu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shooshari, N., Sisson, L., Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S., Usmani, K., Vasquez, L., Vera, Y., Villalón, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wellington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Unpublished
2 (bases 1 to 160505)

Worley, K.C.
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 160505)

Worley, K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:18860158.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KBB
Center clone name: CH230-7M8
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap version 0.990329
Consensus quality: 85656 bases at least Q40
Consensus quality: 89242 bases at least Q30
Consensus quality: 91841 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

* consists of 73 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1078: contig of 1078 bp in length
* 1079 1178: gap of unknown length
* 1179 2301: contig of 1123 bp in length
* 2302 2401: gap of unknown length
* 2402 3565: contig of 1164 bp in length
* 3566 3665: gap of unknown length
* 3666 4836: contig of 1171 bp in length
* 4837 4936: gap of unknown length
* 4937 6418: contig of 1482 bp in length
* 6419 6518: gap of unknown length
* 6519 8010: contig of 1492 bp in length
* 8011 8110: gap of unknown length
* 8111 9241: contig of 1131 bp in length
* 9242 9342: gap of unknown length
* 9343 11003: contig of 1662 bp in length
* 11004 11103: gap of unknown length
* 11104 12448: contig of 1345 bp in length
* 12449 12548: gap of unknown length
* 12549 13795: contig of 1247 bp in length
* 13796 13895: gap of unknown length
* 13896 15042: contig of 1147 bp in length
* 15043 15142: gap of unknown length
* 15143 16474: contig of 1332 bp in length
* 16475 16574: gap of unknown length
* 16575 18485: contig of 1911 bp in length
* 18486 20162: gap of unknown length
* 20163 20262: contig of 1577 bp in length
* 20263 21282: gap of unknown length
* 21283 21382: contig of 1020 bp in length
* 21383 22461: gap of unknown length
* 22462 22561: contig of 1079 bp in length
* 22562 23978: gap of unknown length
* 23979 24078: contig of 1417 bp in length
* 24079 25190: gap of unknown length
* 25191 25290: contig of 1112 bp in length
* 25291 26708: gap of unknown length
* 26709 26808: contig of 1418 bp in length
* 26809 27815: gap of unknown length
* 27816 27915: contig of 1007 bp in length
* 27916 29566: gap of unknown length
* 29567 30945: contig of 1651 bp in length
* 30946 31045: gap of unknown length
* 31046 32586: contig of 1541 bp in length
* 32587 32686: gap of unknown length
* 32687 33767: contig of 1081 bp in length
* 33768 35090: gap of unknown length
* 35091 35190: contig of 1223 bp in length
* 35191 36325: gap of unknown length
* 36326 36425: contig of 1135 bp in length
* 36426 37693: gap of unknown length
* 37694 37793: contig of 1268 bp in length
* 37794 39651: gap of unknown length
* 39652 41554: gap of unknown length
* 41555 41654: contig of 1703 bp in length
* 41655 43208: gap of unknown length
* 43209 43308: contig of 1554 bp in length
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* 44381 44480: contig of 1072 bp in length
* 44481 45849: gap of unknown length
* 45850 45949: contig of 1369 bp in length
* 45950 47477: gap of unknown length
* 47478 47577: contig of 1528 bp in length
* 47578 47677: gap of unknown length


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* 47578 48807: contig of 1230 bp in length
* 48808 48907: gap of unknown length
* 48908 50621: contig of 1714 bp in length
* 50622 50721: gap of unknown length
* 50722 52321: contig of 1600 bp in length
* 52322 52421: gap of unknown length
* 52422 54562: contig of 2141 bp in length
* 54563 54662: gap of unknown length
* 54663 56749: contig of 2087 bp in length
* 56750 56849: gap of unknown length
* 56850 58813: contig of 1964 bp in length
* 58814 58913: gap of unknown length
* 58914 60172: contig of 1259 bp in length
* 60173 60272: gap of unknown length
* 60273 61484: contig of 1212 bp in length
* 61485 61585: gap of unknown length
* 61585 63997: contig of 2413 bp in length
* 63998 64097: gap of unknown length
* 64098 65811: contig of 1714 bp in length
* 65812 65911: gap of unknown length
* 65912 68609: contig of 2698 bp in length
* 68610 68709: gap of unknown length
* 68710 69741: contig of 1032 bp in length
* 69742 69841: gap of unknown length
* 69842 71515: contig of 1674 bp in length
* 71516 71615: gap of unknown length
* 71616 73849: contig of 2234 bp in length
* 73850 73949: gap of unknown length
* 73950 75890: contig of 1941 bp in length
* 75891 75990: gap of unknown length
* 75991 77716: contig of 1726 bp in length
* 77717 77816: gap of unknown length
* 77817 79737: contig of 1921 bp in length
* 79738 79837: gap of unknown length
* 79838 82178: contig of 2341 bp in length
* 82179 82278: gap of unknown length
* 82279 85301: contig of 3023 bp in length
* 85302 85401: gap of unknown length
* 85402 88054: contig of 2653 bp in length
* 88055 88154: gap of unknown length
* 88155 89824: contig of 1670 bp in length

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```

Query Match      83.6% Score 18.4: DB 2: Length 160505;
Best Local Similarity 95.0% Pred. No. 3.1e+02;
Matches 19: Conservative 0; Mismatches 1: Indels 0; Gaps 0;

```

```

QY 2 TGATCTGCAAGATGACTCA 21
||||| |||||||||
Db 102916 TGATCTTCAAGATGACTCA 102935

```

```

RESULT 6
AC123249/c 163363 bp DNA linear HTG 18-JUL-2002
LOCUS Rattus norvegicus clone CH230-24AB19, *** SEQUENCING IN PROGRESS
DEFINITION
AC123249
***, 44 unordered pieces.
AC123249 2 GI:21671666
HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 163363)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsdorcks,S.L., Amaral-tunje,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbatai,J., Benton,J., Bimagne,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

```

COMMENT

```

David,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C., Elhaj,C., Escoto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garra,N., Gill,R.,
Gorrell,D.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsli,F., Howard,S., Huber,J., Huylk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kuresh,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtharge,O., Lieu,C., Liu,J., Liu,W., Louisedge,H.,
Lozato,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Oguh,M., Okwuon,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoshari,N., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,Y., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 163363)
Worley,K.C.
Direct Submission
Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 163363)
Worley,K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 2, 2002 this sequence version replaced gi:21240087.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GTPN
Center clone name: CH230-24AB19
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 126344 bases at least Q40
Consensus quality: 131142 bases at least Q30
Consensus quality: 134321 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 1503: contig of 1503 bp in length
* 1504: gap of unknown length
* 1603: contig of 1427 bp in length
* 3030: gap of unknown length
* 3130: gap of unknown length
* 3131: 4392: contig of 1262 bp in length
* 4393: 4492: gap of unknown length
* 4493: 4582: contig of 1360 bp in length
* 5853: 5952: gap of unknown length
* 5953: 6995: contig of 1043 bp in length
* 6996: 7095: gap of unknown length
* 7096: 8586: contig of 1491 bp in length
* 8587: 8686: gap of unknown length
* 8687: 9990: contig of 1304 bp in length
* 9991: 10090: gap of unknown length
* 10091: 11764: contig of 1674 bp in length
* 11765: 11864: gap of unknown length
* 11865: 13429: contig of 1565 bp in length
* 13430: 13529: gap of unknown length
* 13530: 14810: contig of 1281 bp in length
* 14811: 14910: gap of unknown length
* 14911: 16558: contig of 1648 bp in length
* 16559: 16558: gap of unknown length
* 16559: 18315: contig of 1657 bp in length
* 18316: 18415: gap of unknown length
* 18416: 20154: contig of 1739 bp in length
* 20155: 20254: gap of unknown length
* 20255: 22329: contig of 2075 bp in length
* 22330: 22430: gap of unknown length
* 22430: 24344: contig of 1915 bp in length
* 24345: 24444: gap of unknown length
* 24445: 26087: contig of 1643 bp in length
* 26088: 26187: gap of unknown length
* 26188: 28711: contig of 2524 bp in length
* 28712: 28811: gap of unknown length
* 28812: 31094: contig of 2283 bp in length
* 31095: 31194: gap of unknown length
* 31195: 34176: contig of 2982 bp in length
* 34177: 34276: gap of unknown length
* 34277: 36318: contig of 2042 bp in length
* 36319: 36418: gap of unknown length
* 36419: 38416: contig of 1998 bp in length
* 38417: 38516: gap of unknown length
* 38517: 40712: contig of 2196 bp in length
* 40713: 40812: gap of unknown length
* 40813: 43142: contig of 2330 bp in length
* 43143: 43242: gap of unknown length
* 43243: 46103: contig of 2861 bp in length
* 46104: 46203: gap of unknown length
* 46204: 49350: contig of 3147 bp in length
* 49351: 49450: gap of unknown length
* 49451: 51585: contig of 2135 bp in length
* 51586: 51685: gap of unknown length
* 51686: 54333: contig of 2648 bp in length
* 54334: 54433: gap of unknown length
* 54434: 57387: contig of 2954 bp in length
* 57388: 57487: gap of unknown length
* 57488: 59609: contig of 2122 bp in length
* 59610: 59709: gap of unknown length
* 59710: 61392: contig of 1683 bp in length
* 61393: 61492: gap of unknown length
* 61493: 64948: contig of 3456 bp in length
* 64949: 65048: gap of unknown length
* 65049: 69695: contig of 4647 bp in length
* 69696: 69795: gap of unknown length
* 69796: 73662: contig of 3867 bp in length
* 73663: 73762: gap of unknown length
* 73763: 78216: contig of 4454 bp in length
* 78217: 78316: gap of unknown length
* 78317: 83265: contig of 4949 bp in length
* 83266: 83365: gap of unknown length
* 83366: 87882: contig of 4517 bp in length
* 87883: 87982: gap of unknown length
* 87983: 94335: contig of 6353 bp in length

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* 94336 94435: gap of unknown length
* 94436 101393: contig of 6558 bp in length
* 101394 101493: gap of unknown length
* 101494 108508: contig of 7015 bp in length
* 108509 108608: gap of unknown length
* 108609 116416: contig of 7808 bp in length
* 116417 116516: gap of unknown length
* 116517 121947: contig of 5431 bp in length
* 121948 122047: gap of unknown length
* 122048 136820: contig of 14773 bp in length
* 136821 136920: gap of unknown length
* 136921 149385: contig of 12465 bp in length
* 149386 149485: gap of unknown length
* 149486 163363: contig of 13878 bp in length.
Location/Qualifiers
1. 163363
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-244B19"

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BASE COUNT 50158 a 29064 c 29515 g 48662 t 5964 others
ORIGIN
Query Match 83.6%; Score 18.4; DB 2; Length 163363;
Best Local Similarity 95.0%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 3 GATCTGCAAGATGAACTCAC 22
Db 4638 GATCTGAAAGATGAACTCAC 4619

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RESULT 7
AC025613 172475 bp DNA linear PRI 02-SEP-2000
DEFINITION Homo sapiens chromosome 3 clone RP11-514J23, complete sequence.
AC025613
VERSION AC025613.14 GI:9964950
KEYWORDS HTG.
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE
AUTHORS Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federpiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
Unpublished
2 (bases 1 to 172475)
JOURNAL
REFERENCE
AUTHORS Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federpiel,N.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.
Direct Submission
Submitted (12-MAR-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

```

```

TITLE
JOURNAL
AUTHORS 3 (bases 1 to 172475)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federpiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
Direct Submission
Submitted (02-SEP-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

```

```

COMMENT
On Sep 2, 2000 this sequence version replaced gl:8671904.
----- Genome Center

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```

Center: Stanford DNA Sequencing and Technology Development
Center code: SDSFDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu

```

```

----- Project Information -----
Center project name: 856
Center clone name: RP11-514J23


----- Summary -----
This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

Location/Qualifiers
    source          1..172475
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /chromosome="3"
                   /clone="RP11-514J23"
                   /clone_1lb="RPCI human BAC library 11"
                   /note="single clone coverage"
misc_feature       77005..77022
BASE COUNT        55683 a 31065 c 30948 g 54779 t
ORIGIN
Query Match      81.8%; Score 18; DB 9; Length 172475;
Best Local Similarity 100.0%; Prcd. NO. 4.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY   4 ATCTGACAGATGAAGTCA 21
Db 145110 ATCTGACAGATGAAGTCA 145127

RESULT 8
LOCUS     AC019063               187282 bp    DNA         linear   PRI 25-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-144H20 from 7, complete sequence.
ACCESSION AC019063
VERSION   AC019063.4    GI:8569822
KEYWORDS  HTC.
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE AUTHORS
TITLE     1 (bases 1 to 187282)
JOURNAL   Toward a complete human genome sequence
AUTHORS   Saitou,N.E. and Waterston,R.
MEDLINE   Genome Res. 8 (11), 1097-1108 (1998)
PUBMED   99063792
PUBMED   9847074
REFERENCE AUTHORS
TITLE     2 (bases 1 to 187282)
JOURNAL   Moserler,D., Kyung,K. and Drone,K.
TITLE     The sequence of Homo sapiens BAC clone RP11-144H20
JOURNAL   Unpublished (2002)
REFERENCE AUTHORS
TITLE     3 (bases 1 to 187282)
JOURNAL   Waterston,R.H.
TITLE     Direct Submission
SUBMITTED (30-DEC-1999) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE AUTHORS
TITLE     4 (bases 1 to 187282)
JOURNAL   Waterston,R.H.
TITLE     Direct Submission
SUBMITTED (16-JUN-2000) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE AUTHORS
TITLE     5 (bases 1 to 187282)
JOURNAL   Waterston,R.
TITLE     Direct Submission
SUBMITTED (30-SEP-2000) Department of Genetics, Washington
UNIVERSITY, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE AUTHORS
TITLE     6 (bases 1 to 187282)
JOURNAL   Waterston,R.

```

```

TITLE      Direct Submission
JOURNAL    Submitted (25-JAN-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT    On Jun 16, 2000 this sequence version replaced gi:7630863.

            -----
            Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: sapiens@watson.wustl.edu
            -----
            Summary Statistics
            Center project name: H_NH0144H20
            -----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NHGRI Chromosome 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/CTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPC1-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pletzer de Jong
and coworkers at the Roswell Park Cancer Institute
(http://dacpac.med.buffalo.edu)
VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-144H20;
actual end is at base position 187282 of RP11-144H20.

FEATURES
Source
Location/Qualifiers
1..187282
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="RP11-144H20"
/clone_id="RPC1-11"
3..22545
/repeat_region
/rpt_family="centromeric"
28729..52647
/rpt_family="centromeric"
52648..56317
/rpt_family="L1"
56318..56471
/rpt_family="L1"
56483..75379
/rpt_family="centromeric"
75380..76379
/rpt_family="ERVY"
76380..78367
/rpt_family="centromeric"
78392..78665
/rpt_family="L1"

```


sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality/info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
source	1..226233 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3"
misc_feature	/clone="RP11-484E7" complement(1..2004) /note="Overlaps bases 1..2004 of clone AC024256" /function="clone overlap" complement(578..646) /rpt_family="L2"
repeat_region	813..1003 /rpt_family="L2"
repeat_region	1880..2018 /rpt_family="L1PA5"
STS	1880..2018 /standard_name="150150"
repeat_region	2315..2343 /rpt_family="AT_rich"
repeat_region	2464..2495 /rpt_family="L1PA5"
repeat_region	2700..2724 /rpt_family="TC)n"
repeat_region	2726..2833 /rpt_family="TC)n"
repeat_region	complement(2848..3157) /rpt_family="AluX"
repeat_region	3823..3846 /rpt_family="AT_rich"
repeat_region	4725..4970 /rpt_family="MIR"
repeat_region	complement(5370..5539) /rpt_family="L1M4"
repeat_region	complement(5755..5904) /rpt_family="AluY"
repeat_region	7691..7713 /rpt_family="AT_rich"
repeat_region	complement(7714..8516) /rpt_family="L1PA16"
repeat_region	complement(8675..8971) /rpt_family="AluX"
repeat_region	10315..10345

repeat_region	/rpt_family="AT_rich"
repeat_region	10456..10478 /rpt_family="TA)n"
repeat_region	complement(10749..11047) /rpt_family="AluSg"
repeat_region	12841..13103 /rpt_family="L1ME"
STS	13380..13658 /standard_name="183639"
repeat_region	complement(14885..15450) /rpt_family="MER68"
repeat_region	15802..15940 /rpt_family="MIR"
repeat_region	complement(16272..16626) /rpt_family="MLT2A"
repeat_region	17272..17407 /rpt_family="MLT1E1"
repeat_region	17468..17664 /rpt_family="MLT1E1"
repeat_region	complement(17856..18136) /rpt_family="MLT1J1"
repeat_region	complement(18170..18229) /rpt_family="MIR"
repeat_region	complement(18532..18623) /rpt_family="MIR"
repeat_region	complement(19880..19977) /rpt_family="MLT1E2"
repeat_region	19995..20499 /rpt_family="MER75"
repeat_region	complement(20503..20909) /rpt_family="MLT1D"
repeat_region	complement(23244..23404) /rpt_family="MIR"
repeat_region	23687..23709 /rpt_family="AT_rich"
repeat_region	23882..23945 /rpt_family="TA)n"

Query Match

Best Local Similarity 100.0%; Score 18; DB 9; Length 226233;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ATCTCAAGATGAACTCA 21
|||||
Db 87623 ATCTCAAGATGAACTCA 87606

RESULT 10
AX278138 LOCUS 651 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 6 from Patent WO0177151.
ACCESSION AX278138
VERSION AX278138.1 GI:16605208
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Holtzman,D.A., Spiegelman,B.M. and Yoon,C.H.
TITLE Fgry proteins and nucleic acid molecules and uses therefor
JOURNAL Patent: WO 0177151-A 6 18-OCT-2001;
Millennium Pharmaceuticals, Inc. (US) ; DANA-FARBER CANCER
INSTITUTE, INC. (US)
INSTITUTE, INC. (US)

FEATURES	Location/Qualifiers
source	1..651 /organism="Homo sapiens" /db_xref="taxon:9606"
CDS	1..>651 /note="unnamed protein product" /codon_start=1 /protein_id="CAD10531.1" /db_xref="GI:16605209"

ORIGIN 129 a 203 c 203 g 116 t
Query Match 80.9%; Score 17.8; DB 6; Length 651;
Best Local Similarity 90.5%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 1 GTGATCTGCAGATGACTCA 21
Db 91 GTGAACTGCAGATGACTCA 111
RESULT 11
LOCUS AX278136 1143 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 4 from Patent WO0177151.
ACCESSION AX278136
VERSION AX278136.1 GI:16605206
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Holtzman D.A., Spiegelman B.M. and Yoon C.H.
TITLE Fdrg proteins and nucleic acid molecules and uses therefor
JOURNAL Patent: WO 0177151-A 4 18-OCT-2001;
Millennium Pharmaceuticals, Inc. (US) ; DANA-FARBER CANCER
INSTITUTE, INC. (US)
FEATURES
source 1..1143
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS <1..>1143
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD10530.1"
/db_xref="GI:16605207"
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RDCQELFQVGEROSGLFEIQPGSPPLVNCMTSDGQTVIQRHDSVDFNPWEA
YKAGGDPHGEFMIKLEKVSHTGDRNRLAVOLRDMGNAELLOFSVHLCGEPTAS
LQLTAPVAGOLGATVPSPGSLVPESTWDODHLRRDNCKAKSLSGMWPTGCHSNL
NGQYFRSLPQQRKIKKGIKFKTKMGRITPLQATITMLIQPMAAEAS"
BASE COUNT 232 a 373 c 356 g 182 t
ORIGIN
Query Match 80.9%; Score 17.8; DB 6; Length 1143;
Best Local Similarity 90.5%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 1 GTGATCTGCAGATGACTCA 21
Db 565 GTGAACTGCAGATGACTCA 585
RESULT 12
LOCUS AX278135 1218 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 3 from Patent WO0177151.
ACCESSION AX278135
VERSION AX278135.1 GI:16605204
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1

AUTHORS Holtzman D.A., Spiegelman B.M. and Yoon C.H.
TITLE Fdrg proteins and nucleic acid molecules and uses therefor
JOURNAL Patent: WO 0177151-A 3 18-OCT-2001;
Millennium Pharmaceuticals, Inc. (US) ; DANA-FARBER CANCER
INSTITUTE, INC. (US)
FEATURES
source 1..1218
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS 1..>1218
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD10529.1"
/db_xref="GI:16605205"
/translation="MSCAPTAGAALMCAATAVLNSAGCGPVOSKSPFRASMDENNV
AHGLQIQCGLEHAEKTRLSALERLSACGACGTEGPTLPAPESRYDPEV
HSLOTLQKQNSRIQQLFHKVAQOQRLIEKHQIQLQSQFGLDHLKHLDEVAAP
RRKRLPEMAQVDPAHNYSRLRLPDCQELFQVGEROSGLFEIQPGSPPLVNCMT
TSDGQTVIQRHDSVDFNPWEAYKAGGDPHGEFMIKLEKVSHTGDRNRLAVO
LRDMGNAELLOFSVHLCGEPTASLQLTAPVAGOLGATVPSPGSLVPESTWDODH
LRDNCKAKSLSGMWPTGCHSNLNGQYFRSLPQQRKIKKGIKFKTKMGRITPLQ
ATITMLIQPMAAEAS"
BASE COUNT 241 a 401 c 383 g 193 t
ORIGIN
Query Match 80.9%; Score 17.8; DB 6; Length 1218;
Best Local Similarity 90.5%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 1 GTGATCTGCAGATGACTCA 21
Db 640 GTGAACTGCAGATGACTCA 660
RESULT 13
LOCUS AF169312 1413 bp mRNA linear PRI 06-APR-2000
DEFINITION Homo sapiens hepatic angiotensin-related protein (ANGPTL2) mRNA.
ACCESSION AF169312
VERSION AF169312.1 GI:7453533
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1413)
AUTHORS Kim, I., Kim, H.G., Kim, H., Kim, H.H., Park, S.K., Uhm, C.S., Lee, Z.H.
and Koh, G.Y.
TITLE Hepatic expression, synthesis and secretion of a novel
endothelial-cell apoptosis
fibrinogen/angiotensin-related protein that prevents
Biochem. J. 346 Pt 3, 603-610 (2000)
JOURNAL 20164042
MEDLINE 10696885
PUBMED
REFERENCE 2 (bases 1 to 1413)
AUTHORS Kim, I., Kim, H.-G., Moon, S.O. and Koh, G.Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1999) Cardiac Regeneration Group, National
Research Initiatives, Chonbuk University, San 2-20, Keum-Am-Dong,
Chonju 560-180, South Korea
FEATURES
source 1..1413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="embryo"
CDS 1..1413
/gene="ANGPTL2"
/note="HARP"
65..1285
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/note="contains N-terminal coiled-coil domains and
C-terminal fibrinogen-like domain"

/codon_start=1
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/protein_id="AA62868.1"
/db_xref="GI:7453534"
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AHGLIQGCGANTGANTGAPQSAERAGARLSACGACGCTEGSTDLPLAPESRVPEVL
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RKRLPEMAQPVDPAHNYSRLRLPRDCQELFVGERSGLFEIYQSGSPFLVNCMT
SDGCMVTVIOQRHDSVDPNRPMAYKAGFGDPHGFEMLGLEKHSITGDRNSRLAOL
LSDMGNAELLOFVSYHLGEDTAYSLQTLAPVAGOLGATTVPPSGLSVPESTMDQDHL
LRDKNCAKSLSGGMWFGTCSHNLNGOYFRSIPQQRKLLKGIEMKTRGRYPLQAT
TMLIQPMAAEAS"

BASE COUNT 278 a 463 c 444 g 228 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 9; Length 1413;
Best Local Similarity 90.5%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCA 21
|||||
Db 790 GTGACTGCAAGATGACTCA 724

RESULT 14
AX079874 1855 bp DNA Linear PAT 22-FEB-2001
LOCUS Sequence 5 from Patent WO0105971.
DEFINITION AX079874
ACCESSION AX079874
VERSION AX079874.1 GI:13159399
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1855)
AUTHORS Shimkets, R.A. and Fernandes, E.
TITLE Secreted polypeptides and corresponding polynucleotides
JOURNAL Patent: WO 0105971-A 5 25-JAN-2001;
Curagen Corporation (US)
FEATURES
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154..1371
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LSDMGNAELLOFVSYHLGEDTAYSLQTLAPVAGOLGATTVPPSGLSVPESTMDQDHL
LRDKNCAKSLSGGMWFGTCSHNLNGOYFRSIPQQRKLLKGIEMKTRGRYPLQAT
TMLIQPMAAEAS"

BASE COUNT 366 a 586 c 587 g 316 t

ORIGIN

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Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCA 21
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Db 790 GTGACTGCAAGATGACTCA 810

RESULT 15
AF153606 1860 bp mRNA linear PRI 28-JUN-1999
LOCUS AF153606
DEFINITION Homo sapiens angiotensin-related protein mRNA, complete cds.

ACCESSION AF153606
VERSION AF153606.1 GI:5231136
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1860)
AUTHORS Kim, M.K., Kim, Y.H., Seo, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,
Hwang, S.Y., Im, S.U., Jung, E.J., Lee, J.H. and Kim, J.C.
TITLE A catalogue of genes in the human dermal papilla cells as
identified by expressed sequence tags
JOURNAL Unpublished
2 (bases 1 to 1860)
REFERENCES Kim, M.K., Kim, Y.H., Suh, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,
Hwang, S.Y., Im, S.U., Jung, E.J. and Kim, J.C.
Direct Submission
Submitted (24-MAY-1999) Immunology, Kyungpook National University,
School of Medicine, 101 Dongin Dong, Jung Gu, Taegu, Taegu 700-422,
South Korea
FEATURES
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/cell_type="hair dermal papilla"
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TMLIQPMAAEAS"

BASE COUNT 391 a 584 c 573 g 312 t

ORIGIN

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Best Local Similarity 90.5%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCA 21
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Db 790 GTGACTGCAAGATGACTCA 810

Search completed: December 6, 2002, 03:54:50
Job time : 457.792 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 5.2698 Seconds

(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937a-2

Perfect score: 22

Sequence: 1 gtgacatgcgaatgaactcac 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	21	AAA49208 Human tumour necro
2	22	100.0	22	21	AAA48202 Forward PCR primer
3	18.8	85.5	56743	22	AAK68202 Human immune/haema
4	18.8	85.5	56743	22	AAK61760 Human immune/haema
5	17.8	80.9	305	14	AAO39672 Expressed Sequence
6	17.8	80.9	305	14	AAO59084 Human brain Expres
7	17.8	80.9	432	22	ABA08330 Human hepatic angl
8	17.8	80.9	448	23	AA588089 DNA encoding novel
9	17.8	80.9	474	23	AA588094 DNA encoding novel

10	17.8	80.9	651	24	AAO22561 Human FDRG (fibrin
11	17.8	80.9	1143	24	AAO22560 Human mature FDRG
12	17.8	80.9	1218	24	AAO22559 Human FDRG (fibrin
13	17.8	80.9	1221	21	AA297139 Human gene 75 DNA
14	17.8	80.9	1379	21	AA297132 Human secreted pro
15	17.8	80.9	1413	24	ABO88100 Human osteoblast d
16	17.8	80.9	1484	23	AA588098 Human osteoblast d
17	17.8	80.9	1827	21	AA588092 Novel Human protei
18	17.8	80.9	1855	22	AA588092 Novel Human protei
19	17.8	80.9	1858	20	AA588092 Novel Human protei
20	17.8	80.9	1860	24	ABO88099 DNA encoding a hum
21	17.8	80.9	1862	22	AAO22560 Human osteoblast d
22	17.8	80.9	1865	20	AAO22560 Human osteoblast d
23	17.8	80.9	1869	20	AAO22560 Human osteoblast d
24	17.8	80.9	1869	21	AAO22560 Human osteoblast d
25	17.8	80.9	1869	22	AAO22560 Human osteoblast d
26	17.8	80.9	1869	22	AAO22560 Human osteoblast d
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30	17.8	80.9	1873	22	ABK0254 Human osteoblast d
31	17.8	80.9	1879	21	AA245850 Human osteoblast d
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33	17.8	80.9	1879	22	AA245850 Human osteoblast d
34	17.8	80.9	1891	22	AAO8835 Human angiotensin
35	17.8	80.9	1891	22	AAO8835 Human angiotensin
36	17.8	80.9	1891	22	AAO8835 Human angiotensin
37	17.8	80.9	1891	22	AAO8835 Human angiotensin
38	17.8	80.9	1894	20	AAO8835 Human angiotensin
39	17.8	80.9	1894	24	AAO8835 Human angiotensin
40	17.8	80.9	1911	21	AAO8835 Human angiotensin
41	17.8	80.9	1911	21	AAO8835 Human angiotensin
42	17.4	79.1	1931	21	AA297138 Human gene 75 DNA
43	17.4	79.1	361	23	ABV05286 Human secreted pro
44	17.4	79.1	385	23	ABV05286 Human secreted pro
45	17.4	79.1	427	23	ABV44348 Human prostate exp

ALIGNMENTS

RESULT 1

AAA49208

AAA49208 standard; DNA: 22 bp.

22-NOV-2000 (first entry)

Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-CAF.

Human osteoporosis; PCR primer; ss.

Homo sapiens.

WO200032826-A1.

08-JUN-2000.

30-NOV-1999: 99WO-US28403.

30-NOV-1998: 98US-0110268.

(UYDR-) UNIV DREXEL.

Spotila LD:

WPI: 2000-412362/35.

Identifying individuals at risk of developing osteoporosis comprises assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene in a DNA sample from an individual -


```
XX Example 2; Page 11; 21pp; English.
PS
XX The present sequence is a PCR primer for the (CA)16 repeat of intron 4 of
CC the human tumour necrosis factor alpha receptor 2 (TNFR2) gene. It was
CC thought that this intron might contain a polymorphism related to
CC osteoporosis. However, it was shown that this was not so. However, exon
CC 10 contains three polymorphic sites. By determining the genotype of an
CC individual it is possible to identify those at risk of osteoporosis,
CC which is characterised by low bone density and fragile bones, later in
CC life. Those at greatest risk are those who possess allele 1, which is the
CC rarest allele. This is particularly useful as many cases of osteoporosis
CC go undetected at present.
XX
SQ Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 other;
Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGATCTGCAAGATGACTCAG 22
Db 1 GTGATCTGCAAGATGACTCAG 22
RESULT 2
AAA8202
ID AAA8202 standard; DNA: 22 BP.
XX
AC AAA8202:
XX
DT 15-SEP-2000 (first entry)
XX
DE Forward PCR primer for detection of TNFRSF1B intron 4 polymorphism.
XX
KM Tumour necrosis factor: TNF: TNF-R2: TNFRSF1B: PCR primer:
KM tumour necrosis factor receptor superfamily member 1b; human;
KM cardiovascular disease; coronary artery disease;
KM non-insulin dependent diabetes mellitus; neuropathy in NIDDM;
KM essential hypertension; hyperlipidemia; diabetic neuropathy;
KM vasoprotective; antihypertensive; lipid-lowering;
KM chromosome 1p36.2; DIS2834; ss.
XX
OS Homo sapiens.
XX
PN WO200031293-A1.
XX
PD 02-JUN-2000.
XX
PF 25-NOV-1999; 99WO-AU01050.
XX
PR 25-NOV-1998; 98AU-0007323.
XX
PR 25-NOV-1998; 98AU-0007323.
XX
PA (UNSY ) UNIV SYDNEY.
XX
PI Morris BJ:
XX
DR WPI: 2000-400096/34.
XX
XX
PT Method for diagnosing a predisposition to a complex polygenic disease
PT e.g. coronary heart disease, hyperlipidemia and non-insulin-dependent
PT diabetes mellitus comprises assaying chromosome 1 for a genetic marker
PT -
XX
XX Claim 30; Page 3; 50pp; English.
XX
XX A novel method for determining a predisposition in a subject to a
CC complex polygenic disease involves assaying chromosome 1 for a
CC genetic marker indicative of a predisposition to the disease. This
CC method may be used for determining predisposition to cardiovascular
CC disease, coronary artery disease, non-insulin dependent diabetes
CC mellitus, neuropathy in NIDDM, essential hypertension, hyperlipidemia
CC and diabetic neuropathy. The method can be used for testing an
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CC individual with a family history or in the early stages of a complex
CC polygenic disease to ascertain the chance of developing hypertension,
CC neuropathy or lipid disturbances such as high total cholesterol, high
CC low density lipoprotein cholesterol, abnormal apolipoprotein AI and
CC abnormal glycosylated haemoglobin. Once a complex polygenic disease
CC predisposition has been identified the subject can be treated to prevent
CC or reduce the disease or delay its onset. The genetic marker used
CC in the method is DIS2834 and includes a CA repeat region in intron
CC 4 of the tumour necrosis factor receptor superfamily member 1B
CC (TNFRSF1B) gene. The marker is located at chromosome 1p36.2. The
CC present sequence is the forward PCR primer used for detection of
CC the TNFRSF1B intron 4 polymorphism.
XX
SQ Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 other;
Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGATCTGCAAGATGACTCAG 22
Db 1 GTGATCTGCAAGATGACTCAG 22
RESULT 3
AAK68202/C
ID AAK68202 standard; DNA: 56743 BP.
XX
AC AAK68202:
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23014.
XX
KM Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209457.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0217487.
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PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR 14-AUG-2000; 2000US-0224518.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX
DR WPI; 2001-483426/52.
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 23014; 3071pp + Sequence Listing: English.
XX
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (1)
CC amino acid sequences given in AAM82170 to AAM91921. (1) Have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (1)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (1) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (1) by expressing inactive proteins or to
CC supplement the patient's own production of (1). Additionally, (1)
CC polynucleotides may be used to produce the secreted (1), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (1) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
XX
SQ Sequence 56743 BP; 14298 A; 13270 C; 14240 G; 14935 T; 0 other;

Query Match 85.5%; Score 18.8; DB 22; Length 56743;
Best Local Similarity 90.9%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTGATCTGCACAGATGAATCTCAC 22

Db 16373 GTGAACTGCAAGAGAACTCAG 16352
|||||
RESULT 4
ID AAK81760 standard; DNA: 56743 BP.
XX
AC AAK81760;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:36572.
XX
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN W0200157182-A2.
XX
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PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Barash SC, Ruben SM;

XX DR WPI: 2001-483426/52.

XX PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -

PS Disclosure: SEQ ID NO 36572; 3071pp + Sequence Listing; English.

CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.

XX SQ Sequence 56743 BP; 14298 A; 13270 C; 14240 G; 14935 T; 0 other;

Query Match 85.5%; Score 18.8; DB 22; Length 56743;

Best Local Similarity 90.9%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCAC 22
|||||

Db 16373 GTGAACCTGCAAGAACTCAC 16352

RESULT 5

AAQ39672
ID AAQ39672 standard; DNA: 305 BP.

XX AC AAQ39672;

XX DT 20-MAY-1993 (first entry)

XX DE Expressed Sequence Tag human gene marker EST00364.

XX KW expressed sequence tag; human genome project; chromosome;
KW human gene sequencing; PCR mapping; somatic cell hybrids;
KW sublocalisation; gene tagging; tissue typing.

XX OS Synthetic.

XX PT

PN WO9300353-A.

XX PD 07-JAN-1993.

XX PF 19-JUN-1992; 92WO-US05222.

XX PR 20-JUN-1991; 91US-0716831.

XX PR 12-FEB-1992; 92US-0837195.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX PI Adams MD, Venter JC;

XX DR WPI: 1993-036325/04.

XX PT Particular expressed sequence tags from human cDNA - corresponds
PT to transcription prods. of genes, useful for tagging genes,
PT mapping chromosomes and tissue typing

PS Claim 3; Page 96; 199pp; English.

CC This sequence represents an EST (expressed sequence tag) ESTs are
CC markers for human genes actually transcribed in vivo. Unlike the random
CC genomic DNA sequence tagged sites (STSs), ESTs point directly to
CC expressed genes. The use of ESTs could facilitate the tagging of most
CC expressed human genes within a few years at a fraction of the cost of
CC complete genomic sequencing. Using PCR primers AAQ39419-039580 (sequences
CC designed from the ESTs) sublocalisation of an EST can be achieved with
CC panels of fragments from specific chromosomes or pools of large genomic
CC clones in an analogous manner. This sequence represents EST00364.

XX SQ Sequence 305 BP; 65 A; 69 C; 110 G; 59 T; 2 other;

Query Match 80.9%; Score 17.8; DB 14; Length 305;

Best Local Similarity 90.5%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCA 21
|||||

Db 83 GTGAACCTGCAAGAACTCA 103

RESULT 6

AAQ59084
ID AAQ59084 standard; cDNA: 305 BP.

XX AC AAQ59084;

XX DT 16-MAR-1994 (first entry)

XX DE Human brain Expressed Sequence Tag EST00364.

XX KW Gene transcription product; genetic markers; tagging; in vivo;
KW transcription; mapping; locations; chromosomes; chromosomal; ss.

XX OS Homo sapiens.

XX PN WO9316178-A.

XX PD 19-AUG-1993.

XX PF 12-FEB-1993; 93WO-US01294.

XX PR 12-FEB-1992; 92US-0837195.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX PI Adams MD, Moreno RF, Venter CJ;

XX DR WPI: 1993-272882/34.

XX PT Enriched oligonucleotides and corresp. sequences - used as
PT markers for human genes transcribed in-vivo, facilitate tagging

PT		of most human genes
XX		
PS		Example 1; Page 118; 500pp; English.
XX		
CC		The Expressed Sequence Tag was isolated from a human brain cDNA
CC		library as part of a large set of ESTs which can be used as markers
CC		for human genes transcribed in vivo. They can be used to facilitate
CC		tagging of most human genes, for mapping locations of expressed genes
CC		on chromosomes, for individual or forensic identification, for mapping
CC		locations of disease-associated genes, for identification of tissue
CC		type, and for prep. of antisense sequences, probes and constructs.
CC		EST00364 has a "marginal" coding probability as evaluated using the
CC		coding-region prediction program CRM.
CC		See also AA059041-Q61440.
XX		
S0		Sequence 305 BP; 63 A; 70 C; 109 G; 59 T; 4 other:
	Query Match	80.9%; Score 17.8; DB 14; Length 305;
	Best Local Similarity	90.5%; Pred. NO. 74;
	Matches 19; Conservative	0; Mismatches 2; Indels 0; Gaps 0
OY		
	1 GTGATCTCGCAAGTGAACCTCA 21	
Db	83 CTGAACTCGAAGTGACTCTCA 103	
RESULT 7		
ABA08330		
ID	ABA08330 standard; cDNA: 432 BP.	
XX		
AC	ABA08330:	
XX		
DT	11-JAN-2002 (first entry)	
XX		
DE	Human hepatic angiotensin-related protein homologue cDNA, SEQ ID NO:106.	
KW	Human: cytokine; cell proliferation; cell differentiation; growth factor;	
KM	hematopoiesis regulation; tissue growth; immunomodulator; activin;	
KM	Inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;	
KM	Proliferation; metastasis; cancer; tumour; haematopoietic disorder;	
KM	myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;	
KM	chronic inflammatory condition; proliferative retinopathy;	
KM	atherosclerosis; coronary heart disease; arterial ischemia;	
KM	bone disorder; osteoporosis; vascular growth disorder;	
KM	tissue regeneration; wound healing; infection; immune disorder;	
KM	cell culture; drug screening; gene therapy; antiinflammatory;	
KM	antisthmatic; antiarthritic; haemostatic; antihypertensive;	
KM	cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;	
KM	antifungal; vulnerrary; antituber; ss.	
OS	Homo sapiens.	
SN		
PN	MO200157188-A2.	
XX		
DD	09-AUG-2001.	
XX		
PF	05-FEB-2001: 2001WO-US03800.	
PR	03-FEB-2000: 2000US-0496914.	
PR	27-APR-2000: 2000US-0560875.	
XX		
PA	(HYSE-) HYSER INC.	
PI	Tang YT, Liu C, Drmanac RT;	
DR	WPI: 2001-457740/49.	
DR	P-PDB: ABH1086.	
XX		
PT	Human proteins and DNA encoding sequences useful for preventing,	
PT	treating or ameliorating a medical condition in a mammalian subject	
PT	e.g. arthritis and cancer -	
XX		
XS	Claim 1; Page 378; 1963pp; English	

XX	CC	Sequences	ABAI0981-ABBI2330	represent	1350 novel human polypeptides, and
CC	CC	Sequences	ABA08223-ABA09574	represent	nucleic acids encoding them. The
CC	CC	invention	also relates	to vectors and recombinant	host cells comprising a
CC	CC	nucleotide	of the invention,	methods of producing	the novel polypeptides,
CC	CC	antibodies	against the polypeptides,	methods of detecting	the nucleotides
CC	CC	or polypeptides	in a sample, and methods	of identifying compounds	which
CC	CC	bind to polypeptides	of the invention.	Although novel,	many of the
CC	CC	polypeptides	of the invention	have homology to known	proteins, thereby
CC	CC	giving an insight	into their probable	biological activities,	and hence
CC	CC	potential therapeutic	applications. The	polypeptides of the invention	may
CC	CC	have various activities,	including cytokine,	cell proliferation or cell	
CC	CC	differentiation activities;	stem cell growth	factor activity;	
CC	CC	haematopoietic regulatory	activity; tissue growth	activity;	
CC	CC	immunomodulatory activity;	activin- or inhibin-related	activities;	
CC	CC	chemoattract or chemokinetic	activities; haemostatic,	thrombotic or	
CC	CC	thrombolytic activities;	receptor or ligand	activities; or may be	
CC	CC	involved in oncogenesis,	cancer cell proliferation	or metastasis.	
CC	CC	Depending on their	biological activities,	polypeptides and nucleotides	of
CC	CC	the invention	are useful for preventing,	treating or ameliorating	medical
CC	CC	conditions, e.g., by protein	or gene therapy. Such	conditions include	
CC	CC	cancers, haematopoietic	disorders (e.g., myeloid	or lymphoid cell	
CC	CC	disorders), chronic	inflammatory conditions	(e.g., asthma or arthritis),	
CC	CC	proliferative retinopathy,	atherosclerosis, coronary	heart disease,	
CC	CC	arterial ischemia, bone	disorders (e.g., osteoporosis),	and abnormal	
CC	CC	vascular growth. Polypeptides	involved with tissue	regeneration and	
CC	CC	repair (or nucleic acids	encoding them) may be	used to promote	wound
CC	CC	healing (e.g., of burns,	incisions and ulcers),	while those with	
CC	CC	immunomodulatory activities	may be used in the	treatment of viral,	
CC	CC	bacterial and fungal	infections in addition	to immune disorders.	
CC	CC	Polypeptides with growth	factor activity may be	used in cell cultures	to
CC	CC	promote cell growth. For	example, such polypeptides	may be used to	
CC	CC	manipulate stem cells	in culture to give rise	to neuroepithelial cells	
CC	CC	that can be used to	augment or replace	cells damaged by illness,	
CC	CC	autoimmune disease or	accidental damage. The	polypeptides and nucleotides	
CC	CC	may also be used in the	diagnosis of the above	conditions, and in drug	
CC	CC	screening techniques. The	present sequence	represents a cDNA	encoding a
CC	CC	novel human polypeptide	of the invention.		
XX	SO	Sequence	432 BP; 94 A; 119 C; 125 G; 94 T; 0	other:	
XX	XX	Query Match	80.9%; Score 17.8; DB 22; Length 432;		
XX	XX	Best Local Similarity	90.5%; Pred. No. 78;		
XX	XX	Matches 19; Conservative	0; Mismatches 2; Indels 0; Gaps 0;		
QY	1	GGGATCTGCAAGATCAACTCA	21		
DB	321	GTGAAGTGCAGATGACCTCA	341		
RESULT 8					
AA588089/c					
ID	AA588089	standard; cDNA; 448 BP.			
XX	AA588089;				
AC					
XX					
DT	13-FEB-2002	(first entry)			
XX					
DE	DNA encoding novel human	diagnostic protein #23893.			
XX					
KM	Human: Chromosome mapping;	gene mapping; gene therapy;	forensic;		
XX	food supplement; medical	imaging; diagnostic; genetic	disorder; ss.		
OS	Homo sapiens.				
XX					
PN	MO200175067-A2.				
XX					
PD	11-OCT-2001.				
XX					
PF	30-MAR-2001; 2001WO-US08631.				
XX					
PR	31-MAR-2000; 2000US-0540217.				
XX	23-AUG-2000; 2000US-0649167				